Access DB# 18375



SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:			Date:
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Mail Dox and Didg/Room L	ocation:	_ Results Format Preferred	d (circle): PAPER DISK E-MAI
If more than one search is	submitted, please p	rioritize searches in orde	er of need. ************
Include the elected species or stru-	ctures, keywords, synonym y terms that may have a sp	s, acronyms, and registry numb ecial meaning. Give examples	le the subject matter to be searched. ers, and combine with the concept or or relevant citations, authors, etc, if
Title of Invention:	·		
Inventors (please provide full na	mes):		
Earliest Priority Filing Date:		·	
For Sequence Searches Only Plea appropriate serial number.	se include all pertinent infor	mation (parent, child, divisional, d	er issued patent numbers) along with the
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NA Sequence (#)

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Structure (#)

Bibliographic Litigation

Patent Family

Fulltext

Dialog .

Questel/Orbit
Dr.Link ____

Lexis/Nexis

Sequence Systems
WWW/Internet ___

Other (specify)

PTO-1590 (1-2000)

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SUMMARIES

Result No.

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Description

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Daucus carota

Daucus carota

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core

eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

1 (bases 1 to 6695)

De, V.S., Schmidt, E.D., Van, H.G. and Hecht, V.F.

PRODUCTION OF APOMICTIC SEED

Patent: WO 9743427-A 20-NOV-1997;

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1680	gaatgcagcattatctggtcaattggttcctcttggccagttgaaaaatttacaatac	1621	Qy
1620	GCAGTG	1561	Db
1620	agaaattttgttgagttaattttacttaccaacttttatggcgtcatgcagtgatctt	1561	Qy
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                                                                           2 (bases 1 to 1755)
Schmidt, E.D. L., Guzzo, F., Toonen, M.A.J. and de Vries, S.C.
Direct Submission
Submitted (12-MAR-1997) Molecular Biology, Agricultural University
of Wageningen, Dreyenlaan 3, Wageningen 6703 HA, The Netherlands
                                                                                                                                 Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

1 (bases 1 to 1755)
Schmidt, E.D., Guzzo, F., Toonen, M.A. and de Vries, S.C.
A leucine-rich repeat containing receptor-like kinase marks somatic
plant cells competent to form embryos
Development 124 (10), 2049-2062 (1997)
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KSLLKEKKLEMLVDPDLENNYIOTEVEDLIOVALLCTGGSPMERPKMSEVVRMLEGDG
LAEKWDEMQKVEVIHOVVELAPHRTSEWILDSTDNLHAFELSGPR*
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REFERE AUTH	JOUR	AUTH	REFERE	TITL			REFERE			Q.	SOURCE	KEYWOR	VERSIO		F23M19, LOCUS	d the		Qy 5	Db 3	Ωу 5	Db 3	Ωу 5:	Db 3	Qу 5	ω	О У 5	Db 3	Qy 5	Db 3:	ΩУ 5	ъ 3:	Qу 4:	рь 3;	Qy 4:	Db 3:	Оу 4:	Db 3:
FERENCE 3 (bases 1 to 88401) AUTHORS Theologis, A.	AY-1999) Plant Gene Exp CA 94710. USA	AUTHORS Theologis,	JOURNAL Unpublishe FERENCE 2 (bases	Arabidopsis thaliana chromosome 1	Huizar, L., Kim, C., Pal	Lee, J., Liu, A., Li, J., Kremenetskaia, I.,	AUTHORS Vysotskaia, V.S., Schwartz, J.R., Y	Arabidopsis.	Magnolio	Eukaryota; Viridiplantae; Streptophyta	3		ACCESSION AC007454 VERSION AC007454.3 GI:5091613	sequence.	C F23M19 88401 bp DNA BAC TAGE TAGE TAGE TAGE TAGE TAGE TAGE TAGE	л 6	3741		3681 TCTCAATTACTTTGACGTGAAGTGTTTT	5338 gtttgtttgattaaaaatgaaatataacto	3621 TGGAAGTGTTGCTTCGTGTCTCAGAGGT	5278 tggaagtgttgcgtcatgttta	3561 ATTACGAGGTTTCTGTATGACACCGACCGAG	5218 totacgtggtttctgcatgacacctaccgag	3501 GCTCCAGTTTCAAACAGAAGTAGAGATGATAAGTATGGCA	5158 gctg		5098 tgct		5044		4984		4924	3201 GAAAAGTATTGGAACAACTGTTAATGAAAATCAATACAT		
	ression Center, 800 Buchanan			0 5	owley, D., Shinn, P.,	Luros, J., Gonzalez, A.,	oriumi,M., Lenz,C.,	ries, brassic	calca: Brace (Cacaca)	Embryophyta; Tracheophy				1	PLN 17-JUN-1999 F23W19 sequence, complete				TITATGGGTTCATAATTGTT 3740	gttaaggtgttataatttct 5397	ATTAAACATCTTGTGCTCTC 3680	nattaccataacttgccagaa 5337	AGATTGCTTGTGTATCCTTACATGGCCAA 3620	gtatatccatacatggctaa 5277	TTCATCGAAACCTGTTGAG 3	tgcat		ıgaacgaacaccaggtggcga 5157	AAAGTCTACAAGGGACGCTT 3440	aaggtgtataagggacgcct 5097		ttgcaagtcgcaacggatac 5043	GCAGCCGAAGAAGATCCAGA 3320	tcagctgaagaggacccaga 4983	A	tctattgaagcgct 4923	GCCAGCAATTTTGTTTTGCA 3200

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REFERENCE
AUTHORS
TITLE
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JOURNAL
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Direct Submission
Submitted (17-JUN-1999)
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Submitted (04-JUN-1999) Plant
Street, Albany, CA 94710, USA
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Jun 17, 1999 this sequence version
sequence of BAC F23M19 from Arabic
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SVRHCSLFQDRLKDFKMDSKLKAKLQNTCRGFNDPSVVLDQMTPLEVDNQIYKQIKSQ
RGILRIDQNLGLDDSTSRIVSNPALNETLFGERFAEANQINGBIKVLTGNSGBIRTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFHFLGDAILRYFRCRVNLIYNPDSPLYHGVVSRCQILHGRYVATPWLASPHIQTCEL
WHGLLPVFTYYRQLFLISDGGTIALDWLTNSDYLDGSLHNKSEITKEDTTFLAVVIP
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YYKKSSTQYVGNYAVPLLCISALDDFLCTKEAIFWDECRANKNIYLATNHGGHLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement()01n(796. .1116,1205. .1271,1349. .1432, complement()01n(796. .1150,1299. .2047,2166. .2251,2468. 1506. .1636,1794. .1850,1999. .2047,2166. .2251,2468. 2771. .2893,2990. .3079,3154. .3254,3332. .3393,3467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEGLIGSSLWWVRATNEFLGVLSCSPYMHIQKIVDKRSSGSKQEPSINQGPYLNIAE
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                        PVTLVVTQRDLYHELHALDRFEQDYQRKIQEEENPSTAQRGVGDTLAILRTELKSQKK
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Arabidopsis thaliana chromosome 1.
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                                             gene
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CDS
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GLYSFOLERSGNITLKWRTSA IVMHGLINSSFSSNLSSPRISLOTNGVVSIFESNILG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Contains similarity to gi|479356 protein kinase from Zea mays, is a member of the PF|00954 S-locus glycoprotein family and contains a PF|00069 Eukaryotic protein kinase domain."
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24842. .24955,25045. .25117,25210. .25348,25453. .25865,
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ESLYSDESYVISLQLQYRVLRRESWVSKGPLLLTRQLKTNQNPHLPYM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catcgcgatgtaaaagctgcaaatatattattggacgaagaatttgaggctgttgtaggt 5971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcactaggatcttctaggggcctatctaaattgcatgaccattgtgatcccaagattatc 5911
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                                                                                                                                                                                             gttcctttggttaattatttcacatattagtgcttactactttgttgtggccctttgttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATTTCGGGTTAGCCTAGACTTATGGACTATAAAGATACTCATGTCACAACGGCTGTGCGT
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tcttttaggttaaaagccttttgaaagagaaaaagttggagatgctggtcgatcctgacc
                                                   TTAGCACATATCTGGCTATCTCTCAAAAAGCTGATTTATCTGTTCATTTGGTCT-----
                                                                                                ttatttcctgcctgtatttgattcttagtcatgttatgcatattgacctgctttgcaatg
                                                                                                                                                                                                                                                   CTTGCAAGACTGGCGAATGACGATGACGTTATGCTCCTAGATTGGGTA-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F23M19.7"
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/evidence=not_experimental
/product="F23M19.7"
/broduct="F23M19.7"
/db_xref="G1:5091619"
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NPSISHNTLQNGINVYVAELPRSLNYGLIDXYWSSSTPDSRIPSDPDHPTRKTHSPDK
YPPYPENPLIKQYSAETWIMGDLETSPERIGSTSSAKKVTESSDADVVFVPFFATLSAE
MELGNGSFEKKGNEDYGRGQVLDFVKNTKAWKRSNGCDHYVFVDFFATLSAE
MELGNGSFEKKGNEDYGRGQVLDFVKNTKAWKRSNGCDHYVFUTDLYAMBYRE
EIALSILLVVDEGGWFRQDSKSSNGTSLPERIQHTQVSVIKDVIVPYTHLLPRLDLSQ
NQRRHSILTYKGAKHRHGGLIREKLWDLLVNEFGYVMEEGFPNATGREGSIRGMNS
EFCLHPAGDTPTSCRLFDAIGSLCIPYLYSDTIELFEEGIIDYSESTVFASVSDALTP
KWLANHLGRFSEREKETIRSRIAKVQSVFYYDNGHADGIGPIEPNGAVNHIWKKVQQK
VPMYKEAVIREEKRPAGASVPLKCQCI"
complement(43028. 48860)
/gene="F23M19.8"
complement(43028. 48860)
/Gene="F23M19.4523. 45649,45915. 46249,46361. 47119,
47284. 47637,47725. 47869,48023. 48613,48703. 48736,
48815. 48860)
/GENe="F23M19.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Contains similarity to gi|836774 FAB1 protein
Saccharomyces cerevisiae genome gb|D50617."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/protein_id="AAD39608.1"
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/note="Contains similarity to
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Pred. No. 1.5e-56;
0; Mismatches 258;
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Liu,S.X., Lee,J.M., Sakano,H., Yu,G., Jhaveri,A., Lenz,C.,
Liu,S.X., Chin,C., Chiou,J., Choi,E., Gonzalez,A., Howng,B.,
Toriumi,M., Chin,C., Chiou,J., Choi,E., Gonzalez,A., Howng,B.,
KOO,T., Li,J., Liu,A., Pham,P., Vaysberg,M., Altafi,H., Brooks,S.,
Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N.,
Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Nguyen,M., Palm,C.,
Shinn,P., Tambunga,G., Davis,R.W., Ecker,J.R., Federspiel,N.A. and
                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-NOV-1999) Plant Submitted (02-NOV-1999) Plant CA 94710, USA
                                                                                                                                                                                                                                                            Submitted (10-DEC-1999) Plant Gene Expression Center, 800 Street, Albany, CA 94710, USA on Dec 10, 1999 this sequence version replaced gi:6175131.
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Direct Submission
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                                                                                                                 ø
                                                                                                                                                     /organism="Arabidopsis
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
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Score 378.6; DB 8;
Pred. No. 8.7e-56;
0; Mismatches 454;
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Laboratory, John Innes Centre, Co
E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                  Submitted (11-MAR-1999) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                               Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 viewed at: http://websvr.mips.blochem.mpg.de/proj/thal/.
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complement(join(2377. .2571,2755. .2837,3032. .3098,
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                                                                                                                                                                                                                              Location/Qualifiers
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/product="putative protein"
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grlamunillttgemdgliinndvrirspivetyrehtopveckkusgeriken
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signature [VLAIALDHTVYLWDA] [TGGGGGDRTIKFWNT]
[VASAAGDETLRFWNV]"
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complement(4544. .4687)
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SRYLYMAQSPDGCTYASAAGDETLRFWNVFGYPETAKKAAPKAVAEPFSHVNRIR"
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                                                                                                                                 complement (5815.
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                                                                                                                                                                                                                                                    complement(5363.
                                                                                                                                                                                                                                                                                                                             complement(4688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="WD-repeat protein-like
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                                             lement(6423.
>er=5
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9139...9417,9803...9901)

/note="strong similarity to WD-repeat protein -Daucus carota, PII:92253631; Contains Trp-Asp (WD-40) repeats signature [VLATALDHTVYLWDA] [TGGGGGDRTIKEWNT]
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LPSNHSASLHQOPKSVKPRRYIPQTSERTLDAPDIVDDFYLNLLDWGSANVLAITALDH
TYYLMDASTGSTSELVTIDEEKGPVTSLNWADGRHFAVELNKSEVQLUPDSASNQLK
TYYLMDASTGSTSELWTIDEEKGPVTSLNWADGRIRSBIVETYRGHTQEVCGLKWSG
SGQQLASGGNDNVYHIWDRSVASSNSTTQWLHRLEEHTSAVKALAWCPFQANLLATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10668. .12621
/gene="F17M5.40"
complement(join(10668. .10967,11056. .11159,11587. .12457, 12511. .12621))
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VKMAELTGHTSRVLYMAQSPDGCTVASAAGDETLRFWNVFGVPETAKKAAPKAVSEPF
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                                      12884. .14176
/gene="F17M5.50"
12884. .14176
                                                                                                                                                                                                                                                                                                                                 LSLAKRAISPOGFIVFMKRSHVVSKCFLTIFYKWCVKMMLTROEVVMOVDOTKÆEMK
KNIFGARGSGGISTGWKKFVQDNNLREGDVCVFEPANSETKFLHLNVYIFRGEETERT
NNVDPYTISE"
                                                                                                                                                                                                                                                                                                                                                                                       LEENDLLVFKFHGVSEFEVLVFDGQTLCEKPTSYFVRKCGHAEKTKGIIDFNATSSRS
PKRHFNPDDVETTPNQQLVISPPVDNELEDLIDIDLDFDIDKILNPLLVASHTGYEQE
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                      /gene="F17M5.50"
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AACCCACC 50041
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                                                                                                                                                                                                                                                             TAATTACAAAGACGAAGAAGTGGAGCAGCTAATCCAAGTGGCTTTACTCTGCACTCAGAG
                                                                                                                                                                                                                                                                                      caattacattgacacagaagttgagcagcttattcaagtagcattactctgtacccaggg
                                                                                                                                                                                                                                                                                                                                                                         ggttaaaagccttttgaaagagaaaaagttggagatgctggtcgatcctgacctgcagaa
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                                                                                                            GGTGAAAGGGTTGTTAAAAGAGAAGAAATTGGAAGCACTAGTAGATGTTGATCTTCAGGG 50229
                                         tccacatc 6586
                                                                                     AGCTGAGAGATGGGAAGAGTGGCAAAAGGAGGAAATGTTCAGACAAGATTTCAACTACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLRFIDYCYTEKHICWHEIYDFDSDLWTTLDVTPHWYILSNWSCVGGVSLKGWTYWCA
REBNSDGYNHIICFDFTRERFGPLLFLPWNVINNEYEYVTSSCVREGKLAALFGHNDS
YPYELLEIWITTKIBAEMVSWWKFLRIDIEPNNNIMVPFIYGGFFIDEEKKVBALGFBE
EFGRKTFNIIGEDGYFREFDRITFNIIEEAGERAGVNCGSYVCSYVPSLVRIKKPAQG
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We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T1/A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy

clone

This work was supported by the National Science Department of Energy and the US Department of ${\sf A}_{\sf C}$

Agriculture Foundation Peterson, Michael Holmes, and Delwood Richardson

for software and

Address all correspondence

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AC006436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
(ftp://arthur.gpm.cnni.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named affer the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'nypothetical' proteins. Genes encoding tRNAs are predicted by trNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to the bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-DEC-1999) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:4726109. The sequence and annotation of chromosome 2 were merged from thos of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete sequence.
AC006436 AE002093
AC006436.4 GI:6598565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D., Fujii, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Feldblyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M., Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., Vanaken, S.E., Umayam, L., Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H., Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Glenan, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and Woster, T.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402 (6763), 761-768 (1999)
20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter,J.C
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FEATURES
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I PAKSQUAPRILYPCSEQSKSALNIVERIDERRILSEGEVSE JDSDEPTYTMQETET

TQEEEDDAVVDSTPALRESEFRAFKLEVTGSGLSEGYDARLSLKGRNGGGULVLELS

REFYLAANSDVESGLIAEEKKCSSSSSSLGLKNTCRIEVCDVENLGVFRETVELMFEES

NVIIKKPMTMGYVRAIDVLEVVAGIKFSRAVLSCTLKTEAVPFWEDEEEKLRRLIGIY

SFDDAVSEILLARFUSHETENLQDSLSKKLVMSITSCSDVMPRNELKSLVKGLLCKSIX

VYEKBQPEINKEDIYRAGKCCVDSLAKLLFEEGSSSSKKEKPLIESISREVENINML

LEIMIDREIAEEFVEIMGKGRRLVEMHERVSDFVRYEEGMGQTLLTLPVKEQYQVFMEMFR

EARAGLVEAMFKPMLVDFGWLORCKGLDMREVEEGMGQTLLTLPVKEQYQVFMEMFR

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                                                                                                                                                                                                                                                                                                                                                               complement (<14929. .>17114)

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/note="F13111.4; predicted by genscan and genefinder"

complement(join(14929. .15843,16401. .17114))

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/note="Aptypthetical protein"

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TRGLMNPSGFECCYIFHNMAYELHGLLAGNVSIVTGENIKPSYGGDDEAFLRKVIT
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ETGIKTGNLKHKPKSSD"
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/note="F13J11.1"
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1. .65899
complement(18082..20371)
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/note="F13J11.5"
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SPPRNLYLCLRLYLLAFCHRSPEEIEQDEDSNSSYSPFINRINLINPPRRTDALNKPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Sequence from clone F13J11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIYRVVQTVQV"
10367. .1371
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                                                                                                                                                                                                                                                                                                                   /protein_id="AAD28312.1"
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Best Local Similarity
                                                                                                                                                                                          64398 TATTTGTCATATATTTTTGTTTTTGACTGGTTTGTGATTGGTCAGTTGGTAAGTAT 64457
64516 AAAAAGAAAGCATATTGCTCTGGGATCAGCAAGGGGGCTCGCATATTTACACGATCATTG 64575
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                                                                                                                                                                                                                       5716 taatcgtcccacttactttattcagtttgttctgctctctgaatttttgatctgtacattg 5775
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                                          5836 aactagggagaggattgcactaggatcttctaggggcctatctaaattgcatgaccattg 5895
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                                                                                                                                                                                                                                                                                              542;
                                                                                                                                                                                                                                                                                              Conservative
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complement(37457. .37522)

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join(<38993. .39051,39561. .39686,39797. .39989,

40095. .>40208)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAALVAQAERLGSMRCRASRMPRGREWPRVRVPRDGLKSSEITV
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QIMYSDFYTKKLKLYFTTSNQRKHININKKNYILKKNDKKSKKIILKKYEKKVIQYII
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36924. .37497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(<33782. .>34228)
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complement(29932...3
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Sequence 32 from P
A67827
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De, V.S., Schmidt, E.D., Van, H.G. and
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
                                                                                                                                                                                                    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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KLANDDVMLLDWYKGLLKEKKLEMLVDPDLGTNYERRELEGVIVALLCTGQSPMER
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Query Match Best Local S Matches 524 5980 1481 5920 5860 5800 agagcgtcagccatcagaacctccccctgattggccaactagggagaggattgcactagg 1601 6040 1541 1361 AGAGAGGCCACCGTCACAACCTCCGCTTGATTGGCCAACGCGGAAGAGAATCGCGCTAGG 6340 1757 6220 1721 6160 1661 6100 1421 CTCAGCTCGAGGTTTGTCTTACCTACATGATCACTGCGATCCGAAGATCATTCACCGTGA 1480 1938 1878 6460 1818 6400 1758 1757 6280 Local Sinhes 524; atcttctaggggcctatctaaattgcatgaccattgtgatcccaagattatccatcgcga 5919 gttagotaggotcatggattacaaggattacccatgttacgactgctgtaaggggtaccat 6039 tcgccaatggagcggcctaagatgtcagaggtagtccgaatgcttgaaggtgatggcctt aattacattgacacagaagttgagcagcttattcaagtagcattactctgtacccagggt 6459 gttaaaagccttttgaaagagaaaaagttggagatgctggtcgatcctgacctgcagaac ggttaattatttcacatattagtgcttactactttgttgtggccctttgttttatttcc tggttatgggataatgctcctagagctcattactggacagagggcttttgatcttgctcg 6159 CGGTCACATCGCTCCAGAATATCTCTCAACCGGAAAATCTTCAGAGAAAACCGACGTTTT 1660 tgggcacatagctcccgagtacctctcgactggaaagtcatcagagaagaccgatgtctt 6099 GTTGGCAAAGCTTATGGACTATAAAGACACTCACGTGACAACAGCAGTCCGTGGCACCAT 1600 GTGAAAGGATTGTTGAAGGAGAAGAAGCTAGAGATGTTAGTGGATCCAGATCTTCAAACA tgcctgtatttgattcttagtcatgttatgcatattgacctgctttgcaatgtcttttag 6339 GCTAGCTAACGACGACGTCATGTTACTTGACTG-----TCACCAATGGAAAGACCAAAGATGTCTGAAGTTGTAAGGATGCTGGAAGGAGGATGGGCTT Similarity 60.4 24; Conservative 3.7%; Score 250.4; DB 5; Pred. No. 1.5e-33; 0; Mismatches 201; Indels -----G 143; Gaps 1420 5859 6519 1877 6399 1757 1757 6279 1757 1720 1997 6579 1937 ۲.

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tagctcccgagtacctctcgactggaaagtcatcagagaagaccgatgtctttggttatg
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopl
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Structural Analysis of
Unpublished (1998)
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Arabidopsis thaliana
                              Direct Submission
Submitted (02-Apr-1999) to the DDBJ/EMBL/G
Yasukazu Nakamura, Kazusa DNA Research Ing
Gene Structure 2; 1532-3, Yana, Kisarazu,
(E-mail:ynakamu@kazusa.or.jp, Tel:+81-438
Fax:+81-438-52-3934)
                                                                                                                                                         Structural Analysis of Arabidopsis thaliana Unpublished (1999)
2 (bases 1 to 84896)
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 AC002292 120787 bp DNA
Genomic sequence of Arabidopsis
AC002292
AC002292.1 GI:2252639
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/strain="Columbia"
/db_xref="taxon:3702"
/chromosome="3"
/clone="MWL2"
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2 (bases 1 to 120787)

2 (bases 1 to 120787)

Rederspiel, N.A., Davis, R.W., Conway, A.B., Palm, C.J., Conway, A.R., Kurtz, D.B., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Shinn, P., Sun, H., Oji, O., Osborne, B., Shen, Y.K., Toriumi, M., Vyotskaia, V., Theologis, A. and Ecker, J.
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Submitted (05-JUN-1997) Blochemistry,
Sequencing and Technology Center, 855
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                                                                                                                                                                                                                                                                          Submitted (02-OCT-1997) Biochemistry, Sequencing and Technology Center, 855
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Direct Submission
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6 (bases 1 to
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Submitted (09-JUL-1997) Biochemistry,
Sequencing and Technology Center, 855
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Yu,G., Theologis,A. and Ecker,J.
Direct Submission
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Kurtz,D.B., Buehler,E., Dewar,K., Feng,J., Kim,C., L.
Sun,H., Oji,O., Osborne,B., Shen,Y.K., Toriumi,M., V.
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CA 94304, USA
3 (bases 1 to 120787)
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Jul 11, 1997 this sequence
Location/Qualifiers
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                                                   /gene="F8A5.1"
. join(177. .214,632. .
1845. .2159,2256. .25
/gene="F8A5.1"
                                                                                                                              /chromosome="I"
177. .2876
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                                                                                                                                                                  /organism="Arabidopsis
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                                                                        .2526,2788.
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                                                                          2876)
                                                                                            .1152,1283.
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                                                                                             .1479,1617.
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.1761

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RGELERLEKLMNKYERGOIQSIDWLDRLMLKŠLDTIKEOESTKHGSSHLFVVIDFCSF
EHRVVPQESGANLFITAPIGSTNEFYTWWDTELGKTNPSENKOLKARSIDRGIIDRD
LKPSNIERKSIQRVLKYPPTRTILSGDERQLLMERFRESLMSEKRALTKFLRCVEMSDVO
EAKQAIQLMYKNEMIDWCDALELLSPLFESEEWRAYAWSVLERADDEELQCYLLQLVQ
EAKQAIQLMYKNEMIDWCDALELLSPLFESEEWRAYAWSLHDHYYAKFFYSTYELLEENI
IKLFERSDRSCLSQFLVQRALQNIELASFLRWYYAVELHDHYYAKRFYSTYELLEENI
IKLFERWIGEDGYQLWQSLVRQYTELTAQLCSITREVRNYRGNTGVKIEKLRQLLGGLL
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ERSITTSYLQKFBDEHAFFGITATCLDTFIKSCAGYSVITYILGIGDRHLDNLLLTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(9782. .9919,10031. .10178,10275.
10509. .10663,10780. .10917,10991. .11164,11286.
11815. .11396,12047. .12182,12300. .12395,12475.
12803. .12981,13104. .13313,13414. .13572,13659.
13867. .13963,14069. .14180))
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GLKKVKSAPLVVAMLDDVPEBHREILLASQGCVVREIEPVYPDNQVEFAMAYVYLNY
SKLRIUNFEEYSKMIYLDADIQVFDNIDHLFDLSDAYFYAVMDCFCEKTWSHSLQY;
GYCQCCPEKVTWAPEDMESPPPLYFNAGMFYFEPSPLTYESLLQTLEITPPSPFAEQD
FLNMFFEKVYKPIPLVYNLVLAMLMRHPENVELEKVKVVHYCAAGSKPWRYTGEEANM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3171. .4444)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:2462735"
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LYFNKFLPSFYPHLALSALKKIDWKKYGLILANVNDQDGHYFLEWDNFPSYYQIQIAL
HWYHNQYPTRQKNGPGISLLKKGIKNALDNLKAKHEGFILSHSRKICSYVPDLARSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGLSFAKLFSRLFAKKEMRILMVGLDAAGKTTILYKLKLGEIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(8347. .8443,8539. .8657,8941.
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VWDVSCGKTEGLIGGATVLLENSKMONKSGKOKLRLWGGKEADGSFPTSTPGKVPRHE
                                                                                                                                                                                                                                                                                 GRLFHYDFAFILGRDPKPFPPPMKLCKEMYEAMGGAESQYYTRFKSYCCEAYNILRKS
SNLILNLFHLMAGSTIPDIASDPEKGILKLQEKFRLDMDDEACIHFFQDLINESVSAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(9782. .14180)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(8347. .9066)
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                                                                                                                                                                                                                                                      FPQMVETIHRWAQYWR"
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                                                                                       proteins"
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Sg

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Db 108599 TGGGACAGCGAGAGGACTAGTTTACCTACACGAGCAATGTGACCCGAAGATTATACACCG
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                                                                                                                                                       tgggttagctaggctcatggattacaaggatacccatgttacgactgctgtaaggggtac
                                                                                                                                                                                                                                                     CGATGTGAAAGCAGCTAACATTCTGTTAGATGAGGACTTCGAAGCAGTTGTTGGTGATTT
                                                                                                                                                                                                                                                                                           cgatgtaaaagctgcaaatatattattggacgaagaatttgaaggctgttgtaggtgattt
                                                                                                             TGGGTTAGCTAAGCTTCTAGACCATAGAGACTCTCATGTCACAACTGCAGTCCGTGGAAC
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Similarity 68.2%;
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MSRPVNGQPENIYEQISGMIMKYIEPQESIILINVLSAIKHPHRRAYEQARWQEELLER
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KDAVAAIVDQSSGELLALSLKSGLSTITEELIIMSDEEHIAEAISSAAEAIAGSGKGV
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TAVLELNKLPWVMASTGEALMALMOIIGSAKESLLRILVQGDFSEYPDDQNM5CTARL
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YHAHLLIPAFDMKMRTTSYWKIVLRRIVDNLALYLQLSVKSLVNTRFQKEIVAEMVDP
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IRMSRQVDKTGERTLAVVTKADMAPPESLLQKVTADDVSIGLGYICVRNRIGEETYEEA
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/gene="F8A5.7"
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/db_xref="GI:2462737"
/translation="MGGSKKHVVTRTSSPSLAIVQANPHDNREVVPIEAPIISSYNDR
IRPLLDTVDRLRNLNVMREGIQLPTIVVVGDQSSGKSSVLDSLAGISLPRGQGICTRV
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21973. .22091.22335. .22510)
/gene="%985.6"
/note="%similar to "Mx" GTP-binding proteins"
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join(18712. .19
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AF160182
                                                                                                              Actual end is
                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problem such as compressions and repeats; all regions were covered by sequence from more than one subclone
                                                                                                                                                                                                                                                                                                                                                                                                                     MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (17-JUN-1999) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
2 (bases 1 to 134784)
Sun,H., Wohldmann,P., Johnso
The sequence of A. thaliana
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                                                              start of this clone
at 134784 of F17123.
/organism="Arabidopsis t
/cultivar="Columbia"
/db_xref="taxon:3702"
/clone="F17123"
/chromosome="IV"
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Department of Genetics, Washington
St. Louis, MO 63108, USA
e-mail: rwilson@watson.wustl.edu
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                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54953 GACTGGCCAACAAGGAAGCGTGTAGCTTTTGGTTCAGCTCACGGTTTAGAGTATCTACAC 55012
                                                                                                                                                                                        55313 CTTGATCATGTAAGATTGACTTCTTTTACATGCTTT 55348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5828 gattggccaactagggaggaggattgcactaggatcttctaggggcctatctaaattgcat 5887
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hes 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     attactggacagagggcttttgatcttgctcgccttgcgaacgatgatgatgttatgttg 6187
                                                                                                                                                                                                                                                                                                                                                               actggaaagtcatcagagaagaccgatgtctttggttatgggataatgctcctagagctc 6127
                                                                                                                                                                                                                                                                                                                                                                                                                                           acccatgttacgactgctgtaaggggtaccattgggcacatagctcccgagtacctctcg 6067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACAATTTTGAGCCAGTTCTTGGAGATTTCGGTTTAGCTAAGCTTGTGGACACATCTCTG 55132
                                                                                                                                                                                                                         ttggattgggtatgtgtcccgggtgttcctttggtt 6223
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                                                                                                                                                                                                                                                                                                                                                                                                                      ACTCATGTCACAACTCAAGTCCGAGGCACAATGGGGTCACATTGCGCCAGAGTATCTCTGC 55192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAACATTGTAACCCGAAGATCATACACCGCGATCTCAAGGCTGCAAACATACTTTTAGAC
complete sequence. AC005170 AE002093 AC005170.2 GI:6598 HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sato, S., Kotani, H., Nakamura, Y., Kaneko, T., Asamizu, E., Fukar Miyajima, N. and Tabata, S.
Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned PI clones DNA Res. 4 (3), 215-230 (1997)
9747,1969
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                                                                     AC005170 110211 bp
Arabidopsis thaliana
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Nakamura, Y.
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Similarity 65.7%;
60; Conservative
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/strain="Columbia"
/db_xref="taxon:3702"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone-"MBK5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mitsui p1"
16340 c 16159 g 28865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                  GI:6598448
                                                                         chromosome II section 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 178.4; DB 7;
Pred. No. 1.6e-21;
0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 89779;
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                                                                       17-DEC-1999 of 255 of the
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ORGANISM
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                                                                            misc_feature
repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prediction programs including GRAIL
(ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green,
(Intp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green,
(University of Washington), Genescan (Chris Burge,
http://www.cbs.dtu.dk/services/NetGene2/), searches of the
(http://www.cbs.dtu.dk/services/NetGene2/), searches of the
complete sequence against a peptide database and plant EST
databases at TIGR, and manual curations based on those analyses.
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are named
after the database hits. Genes without significant peptide
similarity but with EST similarity are named as 'unknown' proteins.
Genes without protein or EST similarity, that are predicted by two
or more gene prediction programs over most of their length are
annotated as 'hypothetical' proteins. Genes encoding tRNAs are
predicted by tRNAscan-SE (Sean EEG), Cimila Trocate Notes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (13-DEC-1999) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:3738313.
The sequence and annotation of chromosome 2 were merged from those
of the individual clones on this chromosome after removing
overlaps. For detailed information, please see the TIGR web site
(http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C. Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M. Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayan Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6523, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satcshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu. Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thale cress.
Arabidopsis thaliana
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1 (bases 1 to 110211)
                                                                                                                                                                                                                                                                                        Address all correspondence to:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        This work was supported by the National Science Department of Energy and the US Department of Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to the bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes were identified by a combination of three methods: Gene
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                                                                                                                /chromosome="2"
                                    clone F27L4"
                                                                                                                                                                                                                                                                                                                                at@tigr.org.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Foundation
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/rpt_family "(TANA) n" complement(4565. .4612)
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complement(3570.364
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/note="F77";
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complement(join(1549. .2058,2731.
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complement(1549. .3012)
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VTREMFSKESGHVVEETKLRVTYVCSTTTNITSSPRTRRGFIFQCFC"
complement(11332. .11371)
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KNRRESEALEHMCKLLGGGERAKEIAELWREYEENSSPEAKVVKDFDKVELILQALEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Sequence from clone T29E15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="similar to senescence-associated protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="unknown protein"
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8152. .8268,8487. .8786)
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.9582,9709. .9779,9866.
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                       .20537,20617. .20691,20894.
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      53670 CACCTGAGTATCTCTCCACCGGTCAGTCATCTGAGAAAACCGATGTCTTTGGGTTCGGTA 53611
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29302...29885
/gene="At2g23870"
/note="T29E15.7"
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complement(29076. .2914
/rpt_family="POLY_A"
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21145. .21485))
/gene="At2g23840"
/note="unknown protein"
/codon et=="t="""
/codon et==t="""
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/gene="At2g23840"
/note="T29E15.4"
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33162. .35713,35886. .>36147))
/gene="At2g23880"
complement(<31877. .>36147)
/gene="At2g23880"
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msrlkfcarifssysfpykrkkirdldnteknldidedndewdfdgdddgletddhls
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/gene="At2g23860"
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/gene="At2g23850"
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/rpt_family="(TA)n"
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/protein_id="3738318"
/translation="mytuneknycvrpnyglilpkstcklkrkpgpsDmosnekfmigr
vkaspavtakevtletfnkesghlveetklrvtyvcstttnitspprtrnglyfnvfv
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/gene="At2g23860"
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Total number of hits satisfying chosen parameters:
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Copyright (c) 1993 - 2000
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p 13-MAY-1997; E02443.

r 14-MAY-1996; GB-0.10044.

r 14-PSDB; W47013.

r 14-MAY-1996; GB-0.1004.

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r 16-PSDB; W47013.

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Result No.

Score

Query Match

Length

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Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
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Best Local Similarity
Matches 6692; Conserv
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ilarity 100.0%;
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6300	TGCTTACTTGTTGTGGCCCTTTGTTTTTATTTCCTGCCTG	6241	Db	
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6240	ATGTTGTTGGATTGGGTATGTGTCCCCGGGTGTTCCTTTGGTTAATTATTTCACATATTA	6181	Дb	
6240	gttgttggattgggtatgtgtcccgggfgttcctttggttaattatttcacatatta	6181	Qy	
6180	ATGT	6121	дb	
6180	gagctcattactggacagagggcttttgatcttgctcgccttgcgaacgatgatgatgt	6121	Qy	
6120	CTCTCGACTGGAAAGTCATCAGAGAAGACCGATGTCTTTGGTTATGGGATAATGCTCCT	6061	Db	
6120	tctcgactggaaagtcatcagagaagaccgatgtctttggttatgggataatgctcct	6061	γQ	
6060	CCCGAGTA	6001	DD Db	
6060	aaggatacccatgttacgactgctgtaaggggtaccattgggcacatagctcccgagta	6001	Qy	
6000	TTA	5941	Db	
6000	ttggacgaagaatttgaggctgttgtaggtgattttgggttagctaggctcatggatta	5941	Qy	
5940	ATATT	5881	ф	
5940	ttgcatgaccattgtgatcccaagattatccatcgcgatgtaaaagctgcaaatatatt	5881	Qy	
5880	TCCCCCTGATTGGCCAACTAGGGAGAGGATTGCACTAGGATCTTCTAGGGGCCTATCTAA	5821	Db	
5880	cccctgattggccaactagggagaggattgcactaggatcttctaggggcctatctaa	5821	γQ	
5820	TGTACATTGTGATGTCTTGTTTTCATCAAATGTAGAGCGTCAGCCATCAGAACC	5761	ממ	
5820	tgatctgtacattgtgatgtcttgttttcatcaaatgtagagcgtcagccatcagaacc	5761	ν	
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5760	tatggccctgtatataaatcgtcccacttactttattcagttttgtctgctctctgaattt	5701	Qy	
5700	ATTAGTCTTCATAAATCAGAATCTGCCTAGTGAGCTTTACCGACATACTCTAAACCTTTC	5641	Db	
5700	gtcttcataaatcagaatctgcctagtgagctttaccgacatactctaaacctttc	5641	Qy	
5640	TTCAACTTGGAATCATCTTATAATATACTGTGTAAAGTCAGCTGTTGACTTTCATCATTA	5581	Db	
5640	tcaacttggaatcatcttataatatactgtgtaaagtcagctgttgactttcatcatta	5581	Qy	
5580	ACTGGATGCTATGTTTATTCTGCAATTGAATTCTTGCTTCATGTGCCAAAATATATAT	5521	Db	
5580	yatgctatgtttattctgcaattgaattcttgcttcatgtgccaaaatatatat	5521	Qy	
5520	TATCAA	5461	дь	
5520	tratatttctttcttgtatttggttatatgcaaggatttcgagtctaataagttatcaa	5461	VQ	
5460	CAGATCTTATTTCCCATTGCAAGATACCAGTTATTATTGTTTTTTTCTGTAATTGATACCG	5401	D.	
5460	agatcttatttcccattgcaagataccagttattattgttttttctgtaattgataccg	5401	Qγ	
5400	TGTTTGATTAAAAATGAAATATAACTCCCTACACTATGTTAAGGTGTTATAATTTCTGAG	5341	дb	
5400	gtttgattaaaaatgaaatataactccctacactatgttaaggtgttataatttctgag	5341	Qy	
5340	-	5281	В	
5340	tyttycytcatytttaayayytatctcayttacaattaccataacttyccayaaytt	5281	νQ	
5280		5221	dd	
5280	gtggtttctgcatgacacctaccgagcggcttcttgtatatccatacatggctaatgg	5221	Qy	
5220	GCAGTTTCAAACAGAAGTGGAAATGATTAGCATGGCTGTGCATCGAAATCTTCTGCGTCT	5161	dd Db	

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Production of apomictic seeds - useful in plant breeding
Production of apomictic seeds - useful in plant breeding
Claim 21; Pages 47-51; 123pp; English.

CC The sequence is that encoding SERK, a putative receptor kinase.

CC It may be used as part of a method of producing apomictic seeds

CC comprising: (a) transforming plant material with a nucleotide

CC sequence encoding a protein which in active form in a cell or

CC cell membrane renders the cell embryogenic; (b) regenerating

CC plant parts; and (c) expressing the sequence in the vicinity

CC of the embryo sac. The apomictic seeds and embryos thus produced

CC can be developed into plant progeny. This is useful in plant

CC the case that sexual plants are available as crosses with the

CC propagated hybrids and could shorten and simplify the breeding

CC process so that selfing and progeny testing to produce and/or

CC stabilise a desirable gene combination could be eliminated.

CC Apomixis allows plant breeders to develop cultivars with

CC specific stable traits for such characteristics as height,

Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Daucus carota SERK gene.
receptor kinase; apomixis; a
plant breeding; ss.
Daucus carota.
Key
Location/Qua
CDS
94. .1755
                                                                                                                                                                                                                                                                                                                                                 13-MAY-1997; E02443.
14-MAY-1996; GB-011004.
(NOVS) NOVARTIS AG.
De Viles SC, Hecht VFG, S
WPI; 98-086529/08.
                                                                                                                                                                                                                                                                                                                                                                                                20-NOV-1997;
13-MAY-1997;
14-MAY-1996;
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V06571;
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RESULT V06585 ID VI AC VI DT 0: DE A:

V06585 standard; DNA; V06585; 03-AUG-1998 (first e Arabidopsis thaliana;

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gttagctaggctcatggattacaaggatacccatgttacgactgctgtaaggggtaccat
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                                               ccacatcgaacttctgaatggatcctagactcgacagataacttgcatgcttttgaatta
                                                                             TCGCCAATGGAGCGGCCTAAGATGTCAGAGGTAGTCCGAATGCTTGAAGGTGATGGCCTT
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Pred. No. 9.1e
0; Mismatches
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.1e-108;
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apomixis; apomictic; seeds; production; embryos;

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                                                                                                                                                                                                                              Production of apomictic seeds - useful in plant breeding
Claim 26; Pages 64-67; 123pp; English.
CThe sequence is that encoding SERK, a putative receptor kinase.
CI he sequence is that encoding SERK, a putative receptor kinase.
CI it may be used as part of a method of producing apomictic seeds
C comprising: (a) transforming plant material with a nucleotide
Sequence encoding a protein which in active form in a cell or
cell membrane renders the cell embryogenic; (b) regenerating
the transformed material into plants or carpel-containing
plant parts; and (c) expressing the sequence in the vicinity
of the embryo sac. The apomictic seeds and embryos thus produced
can be developed into plant progeny. This is useful in plant
C breeding programs. Controllable and reproducible apomixis provides
many advantages in plant improvement and cultivar development in
the case that sexual plants are available as crosses with the
                                                       Query Match
Best Local Similarity
Matches 903; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS ) NOVARTIS AG.
De Viles SC, Hecht VFG, S
  2197
                                                                                                                       apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
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plant breeding; ds.
Arabidopsis thaliana
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P-PSDB; W47017.
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                                                     Score 387.4; i
Pred. No. 4.1e
0; Mismatches
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No. 4.1e-73;
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              CABACTCTTTTGAGTAAAATCTCGATTGCAAAATCTCTATGCAGCCGAAGAAGATCCAGA
                            tactgtctgtggactttgttttcactgtcattagtttaacttcagctgaagaggacccaga
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Claim 27; Pages 91-95; 123pp; English.

Claim 27; Pages 91-95; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase.

It may be used as part of a method of producing apomictic seeds comprising; (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding stabilise a desirable gene combination could be eliminated.

Apomixis allows plant breeders to develop cultivars with
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis .
Key
CDS
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20-NOV-1997.
13-MAY-1997; I
14-MAY-1996; (
                                                                                                                                                                                                                                                                                                                                                                                                                        receptor kinase; apomixis; plant breeding; ds.
Arabidopsis thaliana.
Key
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03-AUG-1998 (first e
Arabidopsis thaliana
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De Vries SC, Hecht V
WPI; 98-086529/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V06591 standard; cDNA to
                                                                                                                                                                                                                                                    Production of apomictic
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17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ro
Wang G;
WPI; 99-204431/17.
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This invention describes a method for conferring disease resistance plants. The invention describes the use of novel genes and proteins belonging to the oryza longistaminata and oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins be used for enhancing resistance to Xanthomonas in a plant, preferal
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17-JUN-1999
                                                                                                                                 15-NOV-1996 (first entry)
Tomato RRK gene clone TRK1.
Xa21; RRK; disease resistan
tomato receptor kinase 1; T
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                                                                                                                                                                                                                                                                                                          CDNA;
                                                                                                                                    resistance; Xanthomonas;
nase 1; TRK1; transgenic |
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C DNA clones TRKI (T31307) and TRLI (T31308) were isolated from the conferring primers (T31301-06) based on the camplification of tomato cDNA using primers (T31301-06) based on the crice disease resistance xa21 gene (T31300). They belong to the RRK C family of disease resistance genes. TRKI (tomato receptor kinase 1) is present as 1 or 2 copies in the tomato genome and 1 copy maps to the short arm of chromosome 1 in the proximity of a resistance gene to Xanthomonas campestris pv. vesicatoria RXI. It encodes an RKK protein (W03186) that is an important component of plant signal cransduction pathways leading to a defence response. The gene is useful for engineering disease resistance in tomato and other plants. So Sequence 1554 BP; 477 A; 303 C; 348 G; 426 T;
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Best Local Sin
Matches 197;
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17-JAN-1995; US-373374.
07-JUN-1995; US-475891.
29-SEP-1995; US-004645.
(REGC ) UNIV CALIFORNIA.
Ronald PC, Song W, Szab
WPI; 96-354532/35.
p-PSDB; W03186.
                                                   25-FEB-1999.
17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC) UNIV CALIFORNIA.
Hulbert SH, Richter T, RC
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X23532;
17-JUN-1999
Wang G;
WPI; 99-
P-PSDB;
New RRK
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Xa21; receptor kinase-like protein;
plant disease resistance; cassava; m
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                                                                                                                        Lycopersicon esculentum. WO9909151-A2.
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 g G;
; 99-204431/17.
PSDB; W93600.
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This invention describes a method for conferring disease resistance plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from Kinase-like protein (RRK) Xa21 multigene family.
DNA encoding plant morphogenesis regulatory protein - useful to yield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 17pp; Japanese.

The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to yield a plant with, e.g. short stems or altered inflorescence. The MRP acts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the
                                                                                                                                                                                                                                                                                                               709056382-A.
04-MAR-1997.
24-AUG-1995; 216187.
24-AUG-1995; JP-216187.
24-AUG-1995; JP-216187.
(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
(CHIK-) ZH CHIKYU KANKYO SANGYO GIUITSU KENKYU.
WPI: 97-206629/19.
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Arabidopsis thaliana plant morphogenesis regulatory protein cDNA.
Plant; morphogenesis; regulation; short; stem; alteration;
inflorescence; extraneous; gene; expression; transformation;
increase; control; form; length; ds.
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D 04-MAR-1997.
D 04-MAR-1997.
F 24-AUG-1995; 216187.
F 24-AUG-1995; JP-216187.
R 24-AUG-1995; JP-216187.
N GCHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYUSHO.
NA (CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
NA WPI; 97-206629/19.
PT DNA encoding plant morphogenesis regulatory protein - useful to PT yield plants with short series or altered inflorescence PS Claim 6; Pages 12-15; 17pp; Japanese.
Claim 6; Pages 12-15; 17pp; Japanese.
CC The present sequence encodes an Arabidopsis thaliana plant companies of the present sequence of the pre
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                                                                               contraceptive; ss.
Arabidopsis thaliana.
Key
CDS
Property
Location
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Sequence 9295 BP; 2873 A; 1581 C; 1602 G; 3239 T;
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Arabidopsis steroid receptor Binl DNA.
BIN1; steroid receptor; receptor kinase; transgenic plant;
brassinosteroid; disease resistance; crop protection;
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WO9859039-A1.
30-DEC-1998.
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55.7%;
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Pred. No. 1.3e-13;
0; Mismatches 163;
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PS Claim 8; Page 49-52; 72pp; English.

CC This DNA sequence codes for a novel plant steroid receptor kinase,
CC designated Bini (see W97819), which is involved in the pathway for
CC the synthesis of the plant steroid hormone, brassinolide. 18 New
CC Arabidopsis dwarf mutants were identified that lacked the ability
CC to respond to brassinolide, and were named bin mutants. The bini
CC mutations were used to map the gene to a small interval on
CC The Bini polynucleotide was identified within this interval by
CC sequencing the wild-type and mutant alleles of this nucleic acid.
CC overexpression of Bini in transgenic plants provides plants
CC characterised as having enhanced disease resistance, increased
CC plant yield or vegetative biomass and increased seed yield.
CC Expression of Binl, e.g. using antisense oligonucleotides (AON), is
CC used to render plants male-sterile, and to reduce their stature or
CC yield, e.g. for creating dwarf varieties. Since Bini homologues
CC function, Bini, antibodies and AON may be useful as contraceptives,
CC models for studying steroid-receptor interactions or can be used
CC models for therapeutic agents.
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Matches 200
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Chory J, Li J;
WPI; 99-081275/07.
P-PSDB; W97819.
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24-JUN-1997; US-881706.
(SALK ) SALK INST BIOLOGICAL STUDIES
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 X23531 standard;
X23531;
17-JUN-1999 (fin
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Local 5.
200;
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                                                                                                                   GGATGGGTGAA
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4104 BP; 1061 A;
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(first entry)
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                                 CDNA; 3045
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Pred. No. 2.9e
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2.9e-09;
les 168;
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17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ro
20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New RRK polynucleotides and nucleic acid constructs - used for generating transgenic plants resistant to Xanthomonas Claim 12; Page 58-59; ofpp; English.
This invention describes a method for conferring disease resistance plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sattiva receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins
                                                                                                                                                                                                                                                                                   03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clone.
receptor kinase; apomixis; apomictic; seeds; produc
plant breeding; leucine-rich repeat; ss.
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Xa21; receptor kinase-like protein; multigene family; RRK; rice;
plant disease resistance; cassava; maize; tomato; Xanthomonas; s
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Sequence 3045
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99-204431/17.
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                                                                                                                                                                                                                                                                   thaliana
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Schmidt EDL,
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Pred. No. 4.5e-08;
0; Mismatches 161;
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                                                                                                                                                                                                                                                                                                                  production;
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20-NOV-1997; E02443.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG, Schmidt ED.
WPI; 98-086529/08.
P-PSDB; W47018.
P-PSDB; W47018.
Claim 28; Pages 71-73; 123pp; Engling Serk LRR (leucine-rich repeat) seg Sequence 1106 BP; 331 A; 2
                                                                                                                                                                                                                                                                                                                           Arabidopsis
Key
CDS
                                                                                                                                                                                                                                                                                                                                                 v06586;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERR LRR homologous
receptor kinase; apomixis; apomictic; sec
plant breeding; leucine-rich repeat; ss.
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P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1076
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98; Conservative
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142. .798
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                                                                                                                                          Score 74; DB Pred. No. 7.4e 0; Mismatches
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                                                                                                                                                                                                                  English.
                                                                                                                                                                                       sequences.
258 C;
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Best Local :
Query Match
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20-NOV-1997; E02443.
13-MAY-1996; GB-010044.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-086529/08.
P-PSDB; W47022.
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20-N0V-1997; E02443.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG:
De Vries SC, Hecht VFG, S
WPI; 98-086529/08.
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Arabidopsis
Key
CDS
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The sequence is that of an EST clone showing high SERK LRR (leucine-rich repeat) sequences.
Sequence 788 BP; 234 A; 191 C; 156 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V06588 standard; cDNA to mRNA; 788 Bp. V06588; 03-AUG-1998 (first entry) Arabidopsis thaliana SERK LRR homologous receptor kinase; apomixis; apomictic; see plant breeding; leucine-rich repeat; ss.
                                                                     Claim 28; Pages 86-88; 123pp; F
The sequence is that of an EST
SERK LRR (leucine-rich repeat)
Sequence 1063 BP; 313 A;
                                                                                                                                                   Production of apomictic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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Similarity
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Pred. No. 3.2e
0; Mismatches
 Score
Pred.
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T clone showing
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1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/

4: /cgn2_6/ptodata/
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   GenCore version Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
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US-08-447-185-3

GS-08-447-185-3

PCT-US93-06251-77

US-07-928-464-1

PCT-US93-07347-1

US-08-603-311B-1

US-08-602-010A-7

US-08-602-010A-7

US-08-602-010A-2

US-08-602-726A-1

US-08-680-726A-1

US-08-680-726A-51

US-08-680-726A-51

US-08-680-726A-51

US-08-680-726A-51

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US-08-680-726A-51

US-08-680-726A-51
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US-08-473-553A-1

US-07-717-331F-9

US-07-717-331F-4

US-07-717-331F-4

US-08-265-628-1

US-08-232-463-1

US-08-487-826B-13

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US-08-587-680A-24
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APPLICANT: Ronald
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE FORDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CITY: San Francisco
STATE: California
COUNTRY: USA
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	Sequence 62, Appl	Sequence 62, Appl	Sequence 220, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	12,	Sequence 1, Appli	Sequence 36, Appl	Sequence 14, Appl	Sequence 1, Appli	Sequence 1, Appli	•	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli

ALIGNMENTS

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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 34,774
REFERENCE/JOCKET NUMBER: 023070-058
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
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APPLICANT: Scong, Wen-Yuang
APPLICANT: Scabo, Veronique
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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; TOPOLOGY: Linear
; MOLECULE TYPE: CDNA (partial)
US-08-587-680A-24
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Best Local Similarity 60.8
Matches 197; Conservative
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                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
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                                                        ATTORNEY/AGENT INFORMATION:
NAME: $11va, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPAX: (415) 398-3249
                    TELEX: 910 277299
NFORMATION FOR SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
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CITY: San Francisco
STATE: California
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N FOR SEQ ID NO:
CHARACTERISTICS:
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.6e-16;
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US-07-717-331F-9
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US-07-717-331F-9
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Best Local S
Matches 106
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                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717
FILING DATE: June 19th 1991
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: June N
                                                                                                                        TELEFAX: (203)268-1951 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4800 TCATCTTCAATGGGAGACGAGACATAGAGTAGCCGTGGAAGCTGCAAAGGGCTTGTGTA 4859
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                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: George M. Yahwak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4860 TCTTCACCATGATTGTTCACCATTGATCTTGCATAGAGATGTTAAGTCCAATAACATTCT 4919
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NAME/KEY:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 0.9%;
Local Similarity 58.9%;
hes 106; Conservative
                                  TOPOLOGY:
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                                                 STRANDEDNESS:
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                                                                                      CENGTH:
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                                               nucleic acid
DEDNESS: single
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                                                                                      2571
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25 Skytop Drive
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                                                                                                                          9:
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Pred. No. 6.6e-05;
0; Mismatches 74;
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Length 2571;

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                                                                                                                                                                                                                                        TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2833 base pairs
TYPE: nucleic acid
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Best Local Similarity 53.1
Matches 154; Conservative
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                                                          Query Match
Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                                                                                                                       COMPUTER: MacIntesh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: George M. Tahwak
REGISTRATION UNMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEPHONE: (203)268-1951
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APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
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MEDIUM TYPE: Floppy Disk
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5049 gtaccatccttggaagaggtggatttggtaaggtgtataagggacgccttgctgatggct 5108
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A Receptor Protein Kinase Gene TITLE OF INVENTION: Encoded At The Self-Incompatability Locus
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                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                       STRANDEDNESS:
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T: 25 Skytop Drive
Trumbull
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ilarity 53.1%;
Conservative
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Pred. No. 6.2e-05;
0; Mismatches 133;
                                                          Score 61.2; DB 1;
Pred. No. 6.4e-05;
0; Mismatches 133;
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US-07-717-331F-4
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; MOLECULE TYPE:
US-07-717-331F-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2749 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Applic
Patent No. 5484905
                                                                                                                                                                               Query Match 0.9%;
Best Local Similarity 51.7%;
Matches 164; Conservative
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APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
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MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: George M. Tahwak
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: STREET: CITY: Trumbull
CITY: Connecticut
TSA
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5889 accattgtgatcccaagattatccatcgcgatgtaaaagctgcaaatatattattggacg 5948
                                                                                          1886 ATTGGCAAATGAGATTTGATATTATCAATGGTATTGCCCGAGGGCTTCTCTATCTTCACC 1945
                                                                                                                     5829 attggccaactagggagaggattgcactaggatcttctaggggcctatctaaaattgcatg 5888
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/7 FILING DATE: June 19th 1991 CLASSIFICATION: 800
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                                                                                                                                                                               Score 61; DB 1; Length 2749; Pred. No. 7e-05; 0; Mismatches 150; Indels
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US-08-265-628-J
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                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
TELEFAX: 312-707-9155
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2749 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                  TOPOLOGY: 1in
MOLECULE TYPE:
HYPOTHETICAL: 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FORM
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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APPLICANT: Goring, Daphne
TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
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ATTORNEY/AGENT INFORMATION:
NAME: Pochopien Ph.D., Donald J.
REGISTRATION NUMBER: 32,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                      ANTI-SENSE:
PUBLICATION INFORMATION:
                                                               POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0'
FILING DATE: 03-MAR-1992
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                                                                                                                                   ORGANISM:
                                                                                                  INDIVIDUAL ISOLATE:
                             NAME/KEY:
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Suite 3400
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APPLICANT: DORNER,
APPLICANT: SCHEIFL:
APPLICANT: FALKNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14,
                            FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
ETILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                     ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5287
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Alexandria
                                                                                                                                                                                                                                   CLASSIFICATION: 435
                TELEPHONE:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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: ROTHSTEIN, STEVEN J.
THE S-LOCUS RECEPTOR KINASE GENE IN A
THE S-LOCUS RECEPTOR KINASE GENE IN A
SELF-INCOMPATIBLE BRASSICA NAPUS LINE ENCODES
FUNCTIONAL SERINE/THREONINE KINASE
FUNCTIONAL SERINE/THREONINE KINASE
OF THE SECONION OF THE PROM 1 TO 2749
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1800 Diagonal Road,
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(703)836-9300
(703)683-4109
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Pred. No. 8.6e-05;
                                                           30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suite 500
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; CLONE: pTZgpt-Fls
US-08-232-463-14
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US-08-487-826B-13/c
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SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Patent No. 5
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APPLICANT: Sim, K
APPLICANT: Chitni
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/08/487,826B
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TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERVIHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
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APPLICANT: Wellems, Thomas E.
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Local Similarity 1.6%; Pred. No. 0.00023;
hes 6; Conservative 229; Mismatches 141; Indels
                                                                                                                                              COUNTRY:
                                                                                                                                                                                                           ADDRESSEE:
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5993827
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                                                                                                                                                                            SSEE: Knobbe Martens Olson & F: 620 Newport Center Drive Newport Beach
DATE:
                                                                                                                                                              California
                                                                                                                                                                                                                                                                                                                                          Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                                                                                                                                                           Peterson, David S.
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10-SEP-1993
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Best Local Similarity 45.9%;
Matches 345; Conservative
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16212 TTTTTTCTAAAAAAAAAATGAACATATATGTGTATGTATATGTATTTAGGTATTAT 16153
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                                                                                                                                                                                                                                                                                                                 15797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Israelsen, Ned REGISTRATION NUMBER: 29,655 REFERENCE/DOCKET NUMBER: NI TELECOMMUNICATION INFORMATION: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                                                                                                            1593 acttttatggcgtcatgcagtgatcttgggaatgcagcattatctggtcaattggttcct 1652
                                                                                                                                                                                                                                                                                                                                                                                                                   1474 tagttataagttaaaaaaaagcttcctattaattccaagatagaggttca-tttttatagt 1532
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                                     cttggccagttgaaaaatttacaatacttgtaagaccatatcacttggaatgctttagtt 1712
                                                                                                                                                                                                                                                                                                                                   tcagcagttgttcggataatatctatgaagcacttaaaaggctgggcaatttttttgtta 1832
                                                                             TTTATATAAAAATTTTTTTTAATTTTTTTTTTGATAATCTTTTTTCATTTTTTATTCTATCA 15565
                                                                                                              tttatacagcacaatgctttcaatatctgttaaaagtgtgaaaaagttgactttctagct 1772
                                                                                                                                                                                                                                   TTATGTATATATTTTTTTTAACATTTTTTTAATTTTTTT---TTATTTTATGATATAT 15741
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Pred. No. 0.0023;
0; Mismatches 394; Indels 13;
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Gaps

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US-08-447-185-2

: Sequence 2, Application US/08447185

: Patent No. 5648599
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; Sequence 83, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rif
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; TOPOLOGY: lin
; MOLECULE TYPE:
PCT-US93-06251-83
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 83:
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FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DIG19110, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
                    GENERAL INFORMATION:
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MEDICIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                     1498
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
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TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
APPLICANT:
                                                                                                                                                      1558 ATAAAGTCTGATGTCTGGTCATTTGGAATTCTGCAAACAGAACTAGTAAC 1607
                                                                                                                                                                                                                                                                                                            1438 AAAATAGCAGACTTTGGTTTTAGCAAGGTTAATTGAAGACAATGAATACACAGCAAGACAA 1497
                                                                                                                                                                                                                                                                                                                                    5963 gttgtaggtgattttgggttagcttaggctcatggattacaaggatacccatgttacgact 6022
                                                                                                                                                                                                                                                                                                                                                                                       1378 AACTATATTCACCGAGATCTTCGGGCTGCTAATATTCTTGTAGGAGAAAATCTTGTGTGC
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LENGTH: 4517 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%;
Local Similarity 52.2%;
les 120; Conservation
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Tanksley,
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                                      Sequence 3, Application patent No. 5648599 GENERAL INFORMATION:
APPLICANT: Tanksley, Martin, GITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: GOldman Mr., Michael L.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)-263-1000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: ACIDING
STRANDEDNESS:
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Best Local Similarity
Matches 159; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Goldman Mr., Michae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263
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                                                                                                                                                                                                                                                                                                                                                                                                                  323 ATGAGATGATTCTAATTTATAAATACATGGAGAATGGGAACCTCAAGAGACATTT
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TOPOLOGY: unl
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                                                                                                                                                                                                                                          Application US/08447185
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Tanksley, Steven D.
MAITLIN, Gregory B.
WENTION: GENE CONFERRING DISEASE RESISTANCE
VENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PATH
EQUENCES: 5
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Pred. No. 0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Box 1051
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TO AN AVIRULENCE GENE IN PLANT PATH
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NUMBER OF SEQUENCES:

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RESULT 12
PCT-US93-06251-77
; Sequence 77, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing;
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphona)
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphona)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.8%;
Best Local Similarity 53.9%;
Matches 159; Conservative
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2443 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Goldman Mr., Michael I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1000
TELEPAX: (716)-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5010 tttctctgcgagaattgcaagtcgcaacggatacttttagtacca-----tccttggaa 5063
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                                                                                                                                                                                                                                                                                                                                                                   5244 ccgagcggcttcttgtatatccatacatggctaatggaagtgttgcgtcatgttt 5298
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5184 tgattagcatggctgtgcatcgaaatcttctgcgtctacgtggtttctgcatgacaccta 5243
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ADDRESSEE: Michael L. Goldman
                                                                                                                                                                                                                                                                                                                                                                                                                                    326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 TTCCTTTAGTAGATTTGGAGGAAGCAACTAATAATTTTGATCACAAGTTTTTAATTGGAC 208
                                                                                                                                                                                                                                                                                                                                              386 ATGAGATGATTCTAATTTATAAATACATGGAGAATGGGAACCTCAAGAGACATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 ATGGTGTCTTTGGGAAGGTTTACAAGGGTGTTTTGCGTGATGGAGCAAAGGTGGCCCTGA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: double
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STATE: New York
                                     ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTCTCATTTTGCAGACATCCGCATCTGGTTTCATTGATAGGATTCTGTGATGAAAGAA
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USA
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Pred. No. 0.0028;
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                                                                                                                                               Arylphosphonates
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 2647 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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US-07-928-464-1
                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/07928464
Patent No. 5367065
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: Mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 118; Conserv
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION: 516-742-4343
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1912 ATCAAGTCTGACGTGTGGTCTTTTGGAATCTTACTCACAGAGCTGGTCAC 196:
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FILING DATE: 19930630
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                       ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: No. 5367065ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31,
                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gctgtaaggggtaccattgggcacatagctcccgagtacctctcgactggaaagtcatca 6082
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                                                                                                              19103
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BER: 8586
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Pred. No. 0.014;
0; Mismatches 112;
                      Version #1.25
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CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: U

US/07/928,464

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RESULT 14
PCT-US93-07347-1
; Sequence 1, Application PC/TUS9307347
; GENERAL INFORMATION:
; GENERAL INFORMATION:
TOSEPH R.
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; LOCATION:
US-07-928-464-1
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Best Local Similarity 52.8%;
Matches 134; Conservative
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Miller, Suzanne E.

REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2164 TIGGTIGACAAAAATATACAGTCAAGGTITTGTGATTTTTGGTCTCTCGCGATTGAAGGCC 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5939 ttattggacgaagaatttgaggctgttgtaggtgattttgggttagctaggctcatggat 5998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5879 aaattgcatgaccattgtgatcccaagattatccatcgcgatgtaaaagctgcaaatata 5938
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                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                           APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
            CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19930805
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                                                                                                                                                                                                       ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: Norris STREET: One Liberty Place - 46th Floor CITY: Philadelphia STATE: PA
CLASSIFICATION
                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctagagctcattac 6132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCTGCGAGATGAGCCGTCTAATGAAAAGTCAGATGTGTACAGCTTCGGGGTCATCTTG 2340
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                                                                         Version #1.25
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; LOCATION:
PCT-US93-07347-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-003-311B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application Patent No. 5444166
GENERAL INFORMATION:
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Best Local Similarity
Matches 134; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5879 aaattgcatgaccattgtgatcccaagattatccatcgcgatgtaaaagctgcaaatata 5938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-1086
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5939 ttattggacgaagaatttgaggctgttgtaggtgattttgggfttagctaggctcatggat 5998
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CO-postible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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            APPLICATION NUMBER: US/08/003.311B
FILING DATE: January 12, 1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock
ADDRESSEE: No. 54441
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
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CITY: Philadelphia
STATE: PA
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                                                                                                                                                                                                                      ZIP: 19103
                                                                                                                                                                                                                                     COUNTRY:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08003311B
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E: No. 5444166ris
One Liberty Place - 46th Floor
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215-508-3100
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ATTORNEY/AGENT INFORMATION:
NAME: LOT1 Y. Beardell
REGISTRATION NUMBER: 34, 293
REFERENCE/DOCKET NUMBER: UPN-1:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FRANTER: COS
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.8%; Score 50.8; DB 1; Length 3033; Best Local Similarity 52.8%; Pred. No. 0.015; Matches 134; Conservative 0; Mismatches 117; Indels 3
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                        6119 ctagagctcattac 6132
                                                                           2281 GTCCTGCGAGATGAGCCGTCTAATGAAAAGTCAGATGTGTACAGCTTCGGGGGTCATCTTG 2340
                                                                                                    6059 tacctctcgactggaaagtcatcagagaagaccgatgtctttggttatgggataatgctc 6118
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2341 TGGGAGCTTGCTAC 2354
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Search completed: June 23, 2000, 22:41:28 Job time: 40034 sec

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length: 1000000
      4857316 seqs, 2026611650 residues
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Total number Searched:

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Scoring table: Sequence: Run Š

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ORGANISM Glycine max CORGANISM Glycine max Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine: 1 (Dases 1 to 532) AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hiller, L., Rucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,	RESULT 1 AW233982 LOCUS AW233982 S132905.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-1713 5' similar to TR:023921 C33921 SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE. ;, mRNA sequence. ACCESSION AW233982 VERSION AW233982.1 GI:6566309 KEYMORDS EST. SOURCE SOUNDER	A1486439 AN32985 AN32985 AN32985 AN32985 AN32985 AN738544 AN738546 AN738546 AN738546 AN738546 AN738546 AN738546 AN738546 AN73055 AN416897 AN416897 AN416897 AN41088599 AN43103346 AN49103346 AN4910344	Score Match Length DB ID Descript 271 4.0 532 79 AW233982 AW23398 245.2 3.7 656 38 AA738547 AA73884 244.8 3.7 1202 84 B09168 207.6 3.1 555 51 A1728030 A172803 197 2.9 538 62 A1900110 A190011 191 8 2.9 597 51 A1727837 A1727837 191.8 2.9 703 51 A1729440 A172944
Qy 5800 agagegtcagccatcagaacctccccctgattggccaactagggagaggattgcactagg 5859	plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virgin Coryell." BASE COUNT 145 a 92 c 129 g 165 t 1 others ORIGIN Query Match 4.0%; Score 271; DB 79; Length 532; Best Local Similarity 79.9%; Pred. No. 1.2e-42; Matches 319; Conservative 0; Mismatches 80; Indels 0; Gaps	Fax: 314 286 1810 Email: estewatson. wustl.edu This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63314 For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com High quality sequence stop: 403. FEATURES 1.332	McCann, R., Waterston, R. and Wilson, R. TITLE Public Soybean EST Project JOURNAL Unpublished (1999) COMMENT On Feb 18, 1999 this sequence version replaced gi:4297707. Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800

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"Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
"Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
The mRNA was isolated from roots of Glycine max nod' plants generously donated by Dr. Gary Stacey.
ediings were innoculated with Bradyrhizobium cus, strain USDA110 priot to harvest. Stratagene's ynthesis Kit (catalog number 200401) was used to size the cDNA. First-strand synthesis was performed methyl dCTP, hence the ligated cDNA was thylated. A modification of Stratagene's strand synthesis primer was used. An 'anchor' tide (V-A,C, or G) was added to the 3' end of the [GAGAGAGAGAGAGAGAGAGAGAGTAGTCTCCAG(T)18V] to anchor incr at the 5' end of the poly(A) tract. After-strand synthesis, the cDNA ends were filled in with Pfu DNA polymerase, ligated to EcoRI adapters and uently phosphorylated. The XhOI site within the strand synthesis primer was then restricted by ion with XhOI; all XhOI sites in the cDNA would be ted by their hemimethylated status. The cDNA would be ted by their hemimethylated status. The cDNA would be ted by their hemimethylated status. The cDNA would be ted by their hemimethylated status. The cDNA GIDCOBRI Life Technologies' cDNA Size Fractionation gene's pBluescript II XR Predigested vector script II SK(+) that has been digested with EcoRI of, and phosporylated by Stratagene). Both the and blue colonies appear to contain recombinant ds with cDNA inserts, based on size (n-25). This
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lable through: Genome Systems, Inc. 4633 World
Louis, Missouri 63134 For further information
30 or (314) 427-3222 FAX:(888) 919-3324 or (314)
t: clones@genomesystems.com or
.com web site: www.genomesystems.com
once stop: 403.
Qualifiers
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Project
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"taxxon:3847"
NOME SYSTEMS CLONE ID: Gm-c1028-1713"
p="Gm-c1028"
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Score 271; DB 79; Length 532; Pred. No. 1.2e-42; 0; Mismatches 80; Indels
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                                                            agagcgtcagccatcagaacctccccctgattgg---ccaactagggagaggattgcact 5856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tggttatgggataatgctcctagagctcattactggacagagggcttttgatcttgctcg
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aggatcttctaggggcctatctaaattgcatgaccattgtgatcccaagattatccatcg 5916
                                       AGAGCGACAGCAATCTGAGCCACCTGTTAAGTGGGAAACAACAAGAAGAAGGATTGCGCT 143
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Annen,F., Chang,J.-L., Paterson,A.H. and Stockhaus,J.
Characterization of 14 different putative protein kinase cDNA
clones of the C4 plant Sorghum bicolor
Mol. Gen. Genet. 259 (1), 115-122 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA738547 656 bp mRNA EST 17-AUC SBRLK5 Sorghum bicolor cv. TX430 leaf Sorghum bicolor ct SbRLK5 similar to protein kinase, highest similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Universitaetsstrasse 1, 40225 Duesseldorf, Tel: (49)-211-81-14953 Fax: (49)-211-81-14871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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AA738547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Nov 29, 1993 this sequence version replaced gi:636097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stockha@uni-duesseldorf.de
                                                                                                                                                                                                                          /note="Organ: leaf; Vector: Lambda ZAP II; Site_1: Site_2: Xho I; leaf cDNA library from green leaves. unidirectionally cloned" a 145 c 184 g 166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorgnum
                                                                                                                                                                                                                                                                                               /db_xref="taxon:4558"
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/clone_lib="Sorghum bicolor cv. TX430 leaf"
/dev_stage="green"
                                                                                                                                                                                                                                                                                                                                                                             /organism="Sorghum bicolor"
/strain="cv. TX430"
                                                                                                                                                                                                                                                                                                                                                                                                                                  ngth: 1100 Std Error: 0.00 Location/Qualifiers
                                                                                                                               3.7%;
                                                                                                                Score 245.2; DB 38;
Pred. No. 1.1e-37;
O; Mismatches 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctttggttatgggataatgctcctagagctcattactggacagagggcttttgatcttgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATTGGACACATTGCGCCTGAGTACCTATCCACTGGCAAGTCCTCTGAAAAGACTGATGT
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                                                                                                                                                                                                                       Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                    BAC End Sequences at ATGC Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis.

1 (bases 1 to 1202)

newar,K., Buehler,E.,
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                                                                                                                                                                                        High quality sequence start: 76 High quality sequence stop: 704
                                                                                                                                                                                                                                                                      Tel: 215-898-9384
Fax: 215-898-8780
                                                                                                                                                                                                                                                                                                                                      Arabidopsis Thaliana Genome University of Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                    Contact: Ecker J.
                                                                                                                                                                                                                                                                                                                                                                                     Other_GSSs: T2E10-Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               survey sequence.
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                322
                                                                                                                                                                                                                                                                                                                   of Biology, University of Pennsylvania,
                                                                                                                                                                                                                                                       jecker@atgenome.bio.upenn.edu
           /sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: HindIII;
HindIII; Produced by Rod Wing"
1 275 c 238 g 354 t 13 others
                                                                                        /organism="Arabidopsis
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T2E10"
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                                                                            clone_lib="TAMU"
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Query Match
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Score 244.8; DB 84; Pred. No. 1.3e-37; 0; Mismatches 176;

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                                                                                                 On Jun 5, 1998 this sequence ver
Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
                                                                                                                                                                                                                                                                                                                                                                       to (U93048)
carota], mRh
AI728030
AI728030.1
EST.
                                                                                                                                                                                           upland cotton.

Gossyptum hirsutum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core

euhyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core

eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 555)

Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.

ESTs from developing cotton fiber

Unpublished (1999)

On Jun 5, 1988 this sequence version replaced g1:3187310.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AI728030 555 bp mRNA EST 11-JUN-1999
BNLGH19629 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to (U93048)....somatic embryogenesis receptor-like kinase [Daucus
                                                               il: burr@bnlux1.bnl.gov
primer: T3 Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                       , mRNA sequence.
                               Location/Qualifiers
1. .555
/organism-"Gossypium hi
/cultivar-"Acala Maxxa"
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Best Local Similarity 62.2%;
Matches 432; Conservative
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soybean
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/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
/note="Vector: pBluescript II KS+"
a 100 c 147 g 162 t
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Pred. No. 2.2e-30;
0; Mismatches 119;
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GENOME SYSTEMS CLONE ID:
1 SOMATIC EMBRYOGENESIS
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                                                       gggttcgccaatggagcggcctaagatgtcagaggtagtccgaatgcttgaaggtgatgg 6515
                                                                                                                                 AACCAACTATATAGAAACTGAGGTAGAACAGTTAATCCAGGTTGCACTACTCTGCACACA
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   AGGTTCCCCGATGGACCGACCTAAGATGTCAGAAGTGGTGAGAATGCTTGAAGGTGATGG
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Seq primer: -40RP from Gibco
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae;
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Location/Qualifiers
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from the apical shoots of 9 to 10 day old etiolated seedlings. The shoot tips including any emerged leaves were harvested for mRNA isolation. The CDNA library was prepared using the Stratagene pBluescript II XR CDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."

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seedlings"
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/db_xref="taxon:3847"
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73.6%;
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Pred. No. 2.4e-28;
0; Mismatches 90;
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Query Match 2.9
Best Local Similarity 69.8
Matches 259; Conservative
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                                                                      131 GAAGATTTTGAAGCAGTTGTCGGTGACTTTGGCCTTGCGAAGTTGGTGGATGTGAGGCGG 190
                                                                                                                                                                                                                                                              11 GATTGGCCTCAAAGAAAAAGAATAACCCTAGGTGCAGCATGTGGGCTGGAGTACCTTCAT 70
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1 (bases 1 to 597)
Blewitt,M., Matz,B.C., Davy,D.F. and Burr,B.
ESTs from developing cotton fiber
Onpublished (1999)
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to (U93048) somatic embryogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 516-344-3396
Fax: 516-344-3407
Email: burr@bnlux
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="immature fiber"
/dev_stage="5ix days post anthesis"
/lab_host="XL1-Blue"
/note="Vector: pBluescript II KS+"
/note="Vector: pBluescript II KS+"
/note="Vector: pBluescript II KS+"
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/db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
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Best Local S
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   acccatgttacgactgctgtaaggggtaccattgggcacatagctcccgagtacctctcg 6067
                                                              GAAGATTTTGAAGCAGTTGTCGGTGACTTTGGCCTTGCGAAGTTGGTGGATGTGAGGCGG 190
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossyplum.
1 (bases 1 to 703)
Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
ESTs from developing cotton fiber
Unpublished (1999)
On Jun 5, 1998 this sequence version replaced g1:3188791.
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AI729440
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Fax: 516-344-3407
Email: burr@bnlux1.bnl.gov
Seg primer: T3 Primer.
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Upton, NY 11973, USA
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Similarity 69.8%;
59; Conservative
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/cultivar="Acala Maxxa"
/dubne_lib="Six-day Cotton fiber"
/tlssue_type="Immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XII-Blue"
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pred. No. 2.4e-27;
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   262;
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Lycopersicon esculentum
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnoliophyta; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI486453 471 bp
EST244774 tomato ovary,
CLED8G2, mRNA sequence.
AI486453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
On May 7, 1998 this sequence version replaced
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,M., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato carpel tissue
                                                                                                                                                                                                                                                                                                                                                                      Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU.
Location/Qualifiers
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                    Similarity
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                                                                                                                                        /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; CLED - Tomato Carpel EST Library OligodT: primed a directionally cloned cDNA in vector Landa ZAP II with and 3' ends located at the EcoRI and XhoI sites,
                                                                                                                                                                                                                                                                               /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cled862"
                                                                                                                           respectively.
                                                                                                                                                                                                             /clone_11b-"tomato ovary, TAMU"
/tlssue_type-"carpel"
/dev_stage-"5 days pre-anthesis to 5 days post-anthesis"
/lab_host-"XL1-Blue MRF/"
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Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
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Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Core
euhyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
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A087p60u Hybrid aspen plasmid library Populus tremula
tremuloides cDNA 5', mRNA sequence.
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Seq primer: CGTTGTAAAACGACGGCCAG
High quality sequence stop: 380.
Location/Qualifiers
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Teknikringen 34, S-100 44 STOCKHOLM,
Tel: +46 8 790 8287
Fax: +46 8 24 54 52
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1 (bases 1 to 380)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Biotechnology
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   Cambial region tissues, including developing xylem, the meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. CDNA was prepared and cloned into lambda gt22a. DNA was isolated and subcloned into pBluescript SK using SalI and
                                                                                                    /note="Vector: pBluescript SK; Site_1: Sall; Site_2: Cambial region tissues, including developing xylem, t meristematic cambial zone and the developing and man
                                                                                                                                                                                             /organism-"Populus tremula x Populus tremuloides"
/db_xref-"taxon:47664"
/clone_lib="Hybrid aspen plasmid library"
/tissue_type="Cambial region"
/dev_stage="1.5 m actively growing tree"
/lab_host="E_coli"
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Medicago truncatula
Medicago truncatula
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; endicotyledons; core
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
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The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
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N201132e rootphos(-)
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AW329855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Developmental stage: phosphate starved; Date: 01/23/00; Submitt to the Database of Expressed Sequence Tags (dbEST) on 01/26/00; More information is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harrison,M.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mjharrison@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                          http://chrysie.tamu.edu/medicago'.
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67 c 99 g 102 t
/clone_lib="rootphos(-)"
/tissue_type="roots"
/tissue_type="roots"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK or Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK or Site_1: EcoRI; Site_2:
/note="Toothoot" Site_1: EcoRI; Site_2: EcoRI; Site_2:
/note="Toothoot" Site_1: EcoRI; Site_2: EcoRI; EcoRI; Site_2:
                                                                                                                                                                                             /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="MHRP-24H06"
                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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Pred. No. 8.9e-26)
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Ellis, L.

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attattggacgaagaatttgaggctgttgtaggtgattttggggttagctaggctcatgga 5997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtacctctcgactggaaagtcatcagagaagaccgatgtcttttggttatgggataatgct 6117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATATTTACATGAACAGTGTGATCCAAAGATAATTCACAGAGATGTTAAAAGCAGCAAATAT 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCAGCTTTAGACTGGGCAACAAGGAAGAGAGAATAGCATTAGGAGCAGGAAGAGGGTTACT 128
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                                                       On Dec 15, 177, Lin Contact: Xiaoying Lin Contact: Xiaoying Lin The Institute for Genomic Research The Institute for Dr., Rockville,
                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
euphyllophytes; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                       Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ969360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ969360 714 bp DNA GSS 28-JAN-2000 LERJM53TF LERG Arabidopsis thaliana genomic clone LERJM53, genomic
                                                                                                                            Unpublished (2000)
On Dec 15, 1999 this sequence
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                               Medical Center Dr.,
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301 838 0208
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               at@tigr.org
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Pred. No. 1.5e-25;
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                                                                                                                                version
http://www.tigr.org/tdb/at/at.html
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Class: shotgun
Minobe, Y. and Sasaki, T.
Rice cDNA from root
Unpublished (1995)
Contact: Yuzo Minobe
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
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Oryza sativa.
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1 (bases 1 to 299)
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/db_xref="haxon:3702"
/clone="LERJM53"
/clone=lib="ijerg"
/clone="Tierg"
/clone=lib="ijerg"
/clone="fireg"
/clo
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; endicotyledons; core
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: minobe@rtcs0.riken.go.
                                                                                                                                                                                                                                                                                                                                                                      survey sequence.
B27171
B27171.1 GI:2513137
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
                                                                                                                                          Arabidopsis Genomic
Unpublished (1997)
Other_GSSs: T2E10TR
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1 (bases 1 to 464)

Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D.
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                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
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                                                                                                                              Contact: Steve Rounsley
                                                                                                                                                                                            Use of a BAC End Sequence
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301 838 0208
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/strain="Mipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="R2976_lA"
/clone_lib="Rice root"
/note="Prepared from seedling root. "
54 c 67 g 85 t
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Pred. No. 3.8e-24;
0; Mismatches 76;
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RESULT 1
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            1 (bases 1 to 991)
Annen, F., Chang, J.-L., Paterson, A.H. and Stockhaus, J.
Characterization of 14 different putative protein kinase clones of the C4 plant Sorghum bicolor
Mol. Gen. Genet. 259 (1), 115-122 (1998)
98409267
                                                                                                                                                                                                               AA738544 991 bp mRNA EST 17-AUG-1998 SbrLK2 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cDNA clone SbRLK2 similar to protein kinase, highest similarity to receptor-like protein kinases, mRNA sequence.

AA738544 AA738544.1 GI:3421469
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                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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                                                                                                                 Poaceae;
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Similarity 65.6%;
92; Conservative
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Location/Qualifiers
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/sex="hermaphrodite"
/note="vector: BeloBACII; Site_1: HindIII; Site_2:
HindIII; Produced by Rod Wing"
87 c 115 g 143 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T2E10"
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1993 this
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sequence version replaced gi:636080
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Pred. No. 1.1e-23;
0; Mismatches 135
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REFERENCE
AUTHORS
TITLE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acccatgttacgactgctgtaaggggtaccattgggcacatagctcccgagtacctctcg 6067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gaagaatttgaggctgttgtaggtgattttgggttagctaggctcatggattacaaggat 6007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gaccattgtgatcccaagattatccatcgcgatgtaaaagctgcaaatatattattggac 5947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATTGGTCTGCAAGGAAGCGAGTGGCTATAGGCACAGCTCGTGGACTGGAGTATTTGCAC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gattggccaactagggagaggattgcactaggatcttctagggggcctatctaaattgcat 5887
                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCACTGGTCAGCGAGCCATAGACTTTTCACGTCTGGAGGAAGAAGATGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACATCTGTGACTACTCAGGTCCGTGGAACAATGGGTCACATTGCCCCTGAAGATTTGTCC 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTGGGAAGTCATCCGAGAGAACCGATGTTTTTGGTTACGGCATAATGCTTCTCGAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240;
                                                                                                                                                                                                                                                     AA738545 1435 bp mRNA EST 17-AUG-1998 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cDNA clone SbRLK3 similar to protein kinase, highest similarity to receptor-like protein kinases, mRNA sequence.

AA738545
1 (bases 1 to 1435)
Annen,F., Chang,J.-L., Paterson,A.H. and Stockhaus,J.
Characterization of 14 different putative protein kinase clones of the C4 plant Sorghum bicolor
Mol. Gen. Genet. 259 (1), 115-122 (1998)
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Universitaetsetrasse 1, 40225 Duesseldorf, Germany
Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.
                                                                                                                                                                        Sorghum bicolor
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EST.
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nilarity 68.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: leaf; Vector: Lambda ZAP II; Site_1: Site_2: Xho I; leaf cDWA library from green leaves. unidirectionally cloned; a 194 c 293 g 251 t
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fuer Entwicklungsbiologie und Molekularbiologie
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/clone="SbRLK2"
/clone_lib="Sorghum bicolor cv. TX430 leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sorghum bicolor"
/strain="cv. TX430"
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                     attactggacagagggcttttgatcttgctcgccttgcgaacgatgatgatgt 6180
                                                                                                                                                                                                                                       gaagaatttgaggctgttgtaggtgattttgggttagctaggctcatggattacaaggat 6007
                                                                                         actggaaagtcatcagagaagaccgatgtctttggttatgggataatgctcctagagctc 6127
                                                                                                                                                                                                                                                                                            gaccattgtgatcccaagattatccatcgcgatgtaaaagctgcaaatatattattggac 5947
GTCACTGGTCAGCGTGCCATAGACTTTTCACGTCTGGAGGAAGAAGATGATGT
                                                                        ACTGGGAAGTCATCCGAGAGAACCGATGTTTTTGGTTACGGCATAATGCTTCTCGAGCTA
                                                                                                                                              ACATCTGTGGCTGCTCAGGTCCGTGGAACTATGGGTCACATTGCCCCCTGAATATTTGTCC 1041
                                                                                                                                                                             acccatgttacgactgctgtaaggggtaccattgggcacatagctcccgagtacctctcg 6067
                                                                                                                                                                                                                  GAAGGTTTTGAACCGGTTGTTGGTGATTTCGGCCTTGGCCAAGCTGGTGGATGTACAGAAG 981
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Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98409267
98409267
on Nov 29, 1993 this sequence version replaced g1:636085
Contact: Stockhaus J
Institut fuer Entwicklungsbiologie und Molekularbiologie
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.5%;
Similarity 67.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4558"
/clone="SbRLK3"
/clone="SbRLK3"
/clone="SbRLK3"
/clone="Stage="green"
/dev_stage="green"
/note="Organ: leaf; Vector: Lambda ZAP II; S
/ite_2: Xho I; leaf cDNA library from green
unidirectionally cloned"
a 300 c 389 g 381 t
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Location/Qualifiers
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/strain="cv. TX430"
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Pred. No. 2.9e-23;
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Search completed: June Job time: 27385 sec 23, 2000, 19:05:52

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Listing first 45 summaries
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Maximum DB seq length: 1000000
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                                                            gcaacggatacttttagt-----accatacttggaagaggtggatttggtaaggtgtat
                                                                                                                                                                                                GGAGCAATAGCTGGTGGAGTTGCTGCAGGTGCTGCTTTGCCCTTTGCTGCTGCCAATA
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 GCGAGTGATGGGTTTAGTAACAAGAACATTTTGGGCAGAGGTGGGTTTGGGAAAGTCTAC
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195. .2072
/note="unnamed pro
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Pred. No. 4.5e-199;
0; Mismatches 402;
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RESULT 4
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                                                 A67796
Sequence
A67796
A67796.1
Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
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                                                TCGCCAATGGAGCGGCCTAAGATGTCAGAGGTAGTCCGAATGCTTGAAGGTGATGGCCTT
                                                                                                                                                                                                 TGCCTGTATTTGATTCTTAGTCATGTTATGCATATTGACCTGCTTTTGCAATGTCTTTTAG
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                                                                                                                                                                                                                                                                             CCTTGCGAACGATGATGATGTTATGTTGGATTGGGTATGTGTCCCGGGTGTTCCTTT
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1 (bases 1 to 6695)

De,VLS.; Schmidt,E.D., Van,H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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/db_xref="taxon:4039"
11182 c 1243 g 2421
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1. .6695
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Pred. No. 2.7e-115;
0; Mismatches 18;
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Submitted (01-MAY-1999) Plant Gene Expression Center,
Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vysotskala, V.S., Schwartz, J.R., Yu, G., Toriumi, M., Lenz, C., Liu, S., Lee, J., Liu, A., Li, J., Kremenetskala, I., Luros, J., Gonzalez, A., Altafi, H., Araujo, R., Chao, Q., Conn, L., Conway, A.B., Dunn, P., Hansen, N., Huizar, L., Kim, C., Palm, C., Rowley, D., Shinn, P., Walker, M., Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A. Walker, M., Baliana chromosome 1 BAC F23M19 sequence Unpublished (1999)

2. (bases 1 to 88401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-JUN-1999) Plant Gene Expression Center, 800 St., Albany, CA 94710, USA On Jun 17, 1999 this sequence version replaced gi:4996902. The sequence of BAC F23M19 from Arabidopsis thaliana chrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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4 (bases 1 to 88401)
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AC007454.3 GI:5091613
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                                                                                 /evidence-not_experimental
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NFHGLPPVFTYTRQLFLTSDGGTIALDWLTNSDYLDGSLHNKSEITKEDTTPIAVVIP
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2771.
3638.
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complement(701n(796. .1116,1205. .1271,1349.
complement(701n(796. .1180,1999. .2047,2166. .22
1506. .1636,1794. .1850,1999. .2047,2166. .22
2771. .2893,2990. .3079,3154. .3254,3332. .33
GLTSDSSSAYLKHLAYDTAKTGWNVVISNHRGLGGVSYTSDGFYNAGGTDDIRVVLDY
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KQKLYDKALTIGLQCYAQLHEPOFLRLANWEGIKKSRSIRDFNHATCLVGKFETYDT
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/chromosome="1"
                                                                                                                                                                                                                                          domain
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F23M19 sequence, complete
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SMGLPLLTTEDQEMLADVSKRRKTPGISKSQEFETVAKARLCKHHRLSKSSSHSPMMG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Contains similarity to gi|479356 protein kinase from Zea mays, is a member of the PF|00954 S-Locus glycoprotein family and contains a PF|00069 Eukaryotic protein kinase domain."
                                                                                                                                                                                                                                                                                       KVYYFPOGHIELVSSLSLSLPLFSFSLHLFSLSLLSLSVETSTREELNELQPICDLPS
KLQCRYVAHIELVSSLSLSLPLFSFSLHLFSLSLLSLSVETSTREELNELQPICDLPS
KLQCRYVAHIELVSSLSLSLFLFSLSTRVLTPONENOPRELVNSFTKYLTASD
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ELEKLFDIKGQLQTRNQWEIAFTDSDEDKMLVGDDFWPEFCNMVKKFITQKRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(23307. 23355,23431. 23627,23656. 23751,23850. 2: 24002. 24415,24225. 24309,24401. 24491,24571. 24735, 24842. 249955,25045. 25117,25210. 25348,25453. 25865, 25953. 26140,26231. 26279)
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HSLAVGTVTAALLRMOPHDCFYNVRKLLLCVFYVGCDASILIDSSTPERPSEKSAEANV 
SVRGEEIIDEVKKELEIVCPKTVSCADIVTLAKTRDSIALAGGLNVTNMVALIGGGHSV 
GVAHCSLFQDRLKDPKMDSKLKAKLONTCRGPNDPSVVLDQMTPLEVDNVGIKQIKSQ 
RGILRIDQNLGLDDSTSRIVSNFALNETLFGERFAEAMQIMGEIKVLTGNSGEIRTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(5693. .6732)
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/gene="F23M19.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMMKNKKDTFSTRRPSSVPIIDFDIDRMKALDVIDRVDTIRSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "HSVVI
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Arabidopsis thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLGMLLNYIFRKKQRPTTTSTS
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Arabidopsis thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F23M19.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MESGNVVNAQPELSGIIDGSKSYVYEQLWKLCAGPLCDIPKLGE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .26279
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Query Match
Best Local Similarity
Matches 828; Conserv
                                                                                                           73350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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757 ctgcgagaattgcaagtcgcaacggatacttttag-----taccatacttggaagaggt 810
                                                                                                                                                    697 tttgatgtgccagctgaagaggacccagaagtgcaccttggtcaactgaagaggttttct 756
                                                                                                           TTCTGTGATGCAGCCGAAGAGGACCCTGAGGTTCACTTGGGGCCAGCTTAAGCGGTTCTCT 73291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(36027. .36827)
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complement(36027. .36827)
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TRNKNKPTVLVLLIGILYGLVVAGGASFGFYLYRIRKQPKRLGEPNEAVTLTQQQSSD
ESIVSDESYVISLQLQYRVLRRFSWVSKGPLLLTRQLKTNQNPHLPYM"
40313. .42356
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GAELVYSGDYGDSNTFERLKLDDGNLERYSSASRNSGEVNAHWSAVDQCLYYGYCCN
FGICSYNDTNPICSCPSNNFDFVDVNDRKGCKRVELSDCSGNTTMLDLYHTRLFTY
EDDPNSESFFAGSSFCRANCLSSVLCLASVSMSDGSGNCWQKHPGSFFTGYQMPSVPS
TSYYKVGGPVLNNTLERATKGDDNNSKVHLWIYAVAVLAGLLGLVAVREIGLWWCCCRK
NPRFGTLSSHYTLLEYASGAPVQFTYKELDAFCKEKLGAGGFGTVYRGVLTNRTV
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FLFTDSAKFLTWEYRFNIALGTAKGITYLHEECRDCIVHCDIKPENILVDDNFAKV
SDFGLAKFLIWEYRFNIALGTAKGITYLHEECRDCIVHCDIKPENILVDDNFAKV
SDFGLAKLLMPKDNRYNMSSVRGTRGYLAPEWLANLFITSKSDVYSYGWNLLELVSGK
RNDVYSERKINHKKESIMAVEEFERGNITKALLDTRLESDQTVDMSDVHMAVWTSFWCIQ
EQPLQRPTMGKVVQMLEGITEIKNPLCPKTISEVSFSGNSMSTSHASMFVASGPTRSS
SFSATRSFOTMGITSGGASTRLSEGSNLGS"
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PNSTFSVSFVPSPSPNSFLAAVSFAGSVPIWSAGTVDSRGSLRLHTSGSLRLTNGSGT
TVWDSKTDRLGVTSGSIEDTGEFILLNNRSVPVWSSFDNPTDTIVQSQNFTAGKILRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(43028. .48860)

/gene="F23M19.8"

complement(join(43028. .43288,43400. .43672,43778. .45067,
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47284. .47637,47725. .47869,48023. .48613,48703. .48736,
48815. .48860))

/gene="F23M19.8"

/note="Contains similarity to gi|836774 FAB1 protein from
Saccharomyces cerevisiae genome gb|D50617."
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KWLANHLGRFSEREKETLRSRIAKVQSVFVYDNGHADGIGPIEPNGAVNHIWKKVQQK
VPMYKEAVIRERRKPAGASVPLRCQCI"
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MELGNGKGSFRKKSGNEDYQRQRQVLDFYKNTKAWKRSNGRDHYFYLTDPYAMWHYRE
EIALSILLVYDFGGWFRQDSKSSNGTSLPERIQHTQYSYIKDYIYPTHLLPRLDLSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F23M19.7"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQRRHSLLYFKGAKHRHRGGLIREKLWDLLVNEPGVVMEEGFPNATGREQSIRGMRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                  23.98;
                                                                                                                                                                                                                                             Score 434; DB 8; : Pred. No. 4.3e-87; 0; Mismatches 245;
                                                                                                                                                                                                                                                                                                                Length 88401;
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g g	73290	TRICGGRACTICAAGTRGCARCTGATRGCTTCAGCARGAACAATTTTGGGCCGARG	231
문	73230		171
Qy	871	ttaaagaagaacgaacaccaggtggtgagctgcagtttcaaacagaggtggaaatg	J
Дb	73170	CTTAAAGAAGAGCGAACCCCAGGTGGCGAGCTCCAGTTTCAGACAGA	111
Qy	931	agcatggctgtgcatcgaaatcttctgcgtctacgtggtttctgcatgacaccaacagag 990	J
DЬ	73110	GCATGGCCGTTCACAGAAATCTCCTCAGGCTACGCGGTTTCTGTATGACCCCTACCG	051
Qy	991	<pre>cggcttcttgtatatccatacatggctaatggaagtgttgcgtcgtgtttaag 104</pre>	4
Дb	73050	ATTGCTTGTTTATCCTTACATGGCTAATGGAAGTGT	991
Qy	1044	104	44
Дb	72990	CTTGGAATTTTAACTGTTTGTATCATAAAGTAGAAAGACTCCCACAATGATGTATAAGTG 729	931
Qy	1044	104	44
Дb	72930	TTGTTTTTGATCTTATCCATTTTTAAAACTTTCCAATACAATTGAGTGAG	871
Qy	1044	cctcccttgattggccaactaggaagaggatt 10	95
Дb	72870	ATGATTACAGAACGTCCACCATCACAGTTGCCTCTAGCCTGGTCAATAAGACAGCAAATC 72	811
Qy	1096	cactaggatctgctagggggctttcttatttgcatgaccattgtgatcccaagattatc 11	55
Дb	72810	CATTGCGACCCCAAAATTATT 72	751
Qy	1156	catcgtgatgtaaaagctgcaaatatatttattggacgaagaatttgaggctgttgtaggt 12:	15
рь	72750	ACCGTGATGTGAAAGCTGCTAATATTCTGTTGGACGAGGAATTTGAGGCGGTGGTAGGT 72	691
Qy	1216	agg 12 	75
Дb	72690	ICGGGTTAGCTAGACTTAIGGACTATAAAGATACTCAIGTCACAACGGCTGIGCGI 72	631
Qy	1276	ggtaccttgggctacatagctcccgagtacctctcgactggaaagtcatcagaggaagacc 13:	35
Db	72630	GGACTATTGGACACATTGCTCCTGAGTATCTCTCAACTGGAAAATCTTCAGAGAAAACT 72	571
Qy	1336	gatytetttygttatyggaffatyettatageteattaetggacagagagetfttgat 13	95
ДĎ	72570	ATGTTTTTGGCTACGGGATCATGCTTTTGGAACTGATTACAGGTCAGAGAGCTTTTGAT 72	511
Qy	1396	cttgctcgccttgcgaacgatgatgatgttatgttgttggattg	40
da	72510	CTTGCAAGACTGGCGAATGACGATGACGTTATGCTCCTAGATTGGGTATAACACAGATCT 72	451
VQ	1440	14	40
ф	72450	TTTAGCACATATCTGGCTATCTCTCAAAAAGCTGATTTATCTGTTCATTTGGTCTTCTCA 72	391
ОУ	1440	ggttaaaagccttttgaaagagaaaaagttggagatgctggtcgatcctgacctggagaa 14	99
đđ	72390	GGTGAAAGGGCTTTTGAAGGAGAAGAAGCTGGAGATGCTTGTGGATCCTGACCTGCAAAG 72	331
Qy	1500	caattacattgacacagaagttgagcagcttattcaagtagcattactctgtacccaggg 15	59
뫄	72330	CAATTACACAGAAGCAGAAGTAGAACAGCTCATACAAGTGGCTCTTCTCTGCACACAGAG 72	271
Qy	56	ttogocaatggagoggoctaagatgtcagaggtagtoogaatgcttgaaggtgatggoct 16	19
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JOURNAL REFERENCE
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AUTHORS
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ORGANISM
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KEYWORDS
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ATF17M5/c
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                                                                      exon
                                                                                                                                                       exon
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AL035678
AL035678.1
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Direct Submission

Submitted (11-MAR-1999) MIPS, at the Max-Planck-Institut fuer submitted (11-MAR-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.blochem.mpg.de.pmayer@mips.blochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 96475)

Bevan, M., Rose, M., Hempel, S., Entian, K.-D., Hoheisel, J., Mewes, H.W., Mannhaupt, G., Mayer, K.F.X. and Schueller, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome viewed at: http://websvr.mips.biochem.mpg.de/proj/thal/.
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                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(2377. .2571,2755. .2837,3032. .3098, 3180. .3230,3461. .3574,3668. .3724,3815. .3928) /note-"similarity to Caenorhabditis elegans cosmid, gene T16G1.11, prD:e1349366; contains EST gb:T20620, N65143, T45799, H36819, R65238, N37318"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F17M5.10" complement(2377. .2571)
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/number=3
                                                               complement(3032.
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GSLAWNNHILTTGGMDGLIINNDYRIRSPIVETYRGHTQEVCGLKWSGSGQQLASGGN
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SGQQLASGGNNVVHTWDRSVASSNSTTQWLLRLEEHTSAVKALAWCPFQANLLATGG
GGGDRTIKFWNTHTGACLNSVDTGSQVCSLLWSKNERELLSSHGFTQNQLTLMKYPSM
                                                                                                                                                                                                                                                      complement(join(7856 ..7999,8104 ..8685,8767...9139...9417,9803...9901))
//ote="strong similarity to WD-repeat protein carota, PII:92253631; Contains Trp-Asp (WD-40) signature [VLAIALDHTVYLWDA] [TGGGGGDRTIKFWNT]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNVVHIWDRSVASSNSTTQWLHRLEEHTSAVKALAWCPFQANLLATGGGGGDRTIKFW
NTHTGACLNSVDTGSQVCSLLWSKNERELLSSHGFTQNQLTLWKYPSMVKMAELIGHT
SRVLYMAQSPDGCTVASAAGDETLRFWNVFGVPETAKKAAPKAVAEPFSHVNRIR"
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5815 . .6093,6423 . .6491))
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complement(7856. .7999)
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692 atttctttgatgtgccagctgaagaggacccagaagtgcaccttggtcaactgaagaggt 751
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ilarity 64.1%;
Conservative
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                                                                                                                                                                                                                                                                                                       /gene="£17M5.50"
12884. .14176
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12511. .12621))
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/number=5
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NNVDPVYTISE"
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                                                                                                                                                                                                                                                                           /note-"strong similarity to Arabidopsis thaliana chromosome II BAC (gene T6A23.21), PID:g3786013"
                                                                                                                                                                                                                                                                                                                                                                                  complement (12511.
                                                                                                                                                                                                                                                                                                                                                                                                               complement(12458.
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                                            Score 398; DB 7; Length 96475; Pred. No. 4.8e-79; 0; Mismatches 240; Indels 184;
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1647	8 gaggtagtccgaatgcttgaaggtgatggccttgcagaaaagtgggacgagtggcaaaaa	158	dg
50081		5014	Vo
1587	8 cttattcaagtagcattactctgtacccagggttcgccaatggagcggcctaagatgtca	152	Qy
		5020	dd
1527	8 ttggagatgctggtcgatcctgacctggagaacaattacattgacacagaagttgagcag	146	Qy
50201		5026	Db
1467	0 gyttaaaagccttttgaaagagaaaaag	144	Qy
50261		5032	Db
1440	gttggattg actagactgggtatatacatatatga	142 5038	Db dd
1428	agagettttgatettgetegeettgegaaegatgatgatgt 	36	Qy dd
1368	9 togactggaaagtcatcagagaagaccgatgtctttggttatgggattatgctcttagag	130	Qy
		5050	Db
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1248	9 gacyaagaatttgaggctgttgtaggtgattttgggttagctaggctcatggattacaag	118:	Qy
		5062	Db
1188	9 catgaccattgtgatcccaagattatccatcgtgatgtaaaagctgcaaatatattattg	1129	Qy
		5068	Db
1128	9 cttgattggccaactaggaagaggattgcactaggatctgctagggggctttcttatttg	1069	Qy
		50740	Db
50741	4agagogtcagccatcagaacctccc	1044 50800	dd Vy
- 00	GTATCTCTCATCTTGTGCCTTTTTCTTTGACTGCAATATTTCCGTCCAATGGTTGCCT	86	DЬ
1044	4	1044	Qy
1044	cagageggettettgtatateeataeatggetaatggaagtgttgeg	986	Db Qy
50861		50920	
985	5 tgattagcatggctgtgcatogaaatcttctgcgtctacgtggtttctgcatgacaccaa	926	Qy
		50980	Дъ
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		51040	Db
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51041		51100	Дъ
805	2 tttctctgcgagaattgcaagtcgcaacggatacttttagtaccatacttggaa	752	Qy
51101		51160	Db
51161) ATTACCGTCTTTTTGCAGCTGAAGAGGACCCAGAAGTTCATTTAGGACAACTGAAGAGGT	51220	Db

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REFERENCE
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                                                                                                                                                                                                                                                                      80038 AGCGAACTCCAGGTGGAGAGCTCCAGTTTCAAACAGAAGTAGAGATGATAAGTATGGCAG
                                                                                                                                                                                              79918 TACAAGTGGCGAGTGATGGGTTTAGTAACAAGAACATTTTGGGCAGAGGTGGGTTTGGGA 79977
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nes 787; Conserv
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                                                            aacgaacaccaggtggtgagctgcagtttcaaaacagaggtggaaaatgattagcatggctg 940
                                                                                                                     aggtgtataagggacgccttgctgatggctcacttgtagcagttaaaaggcttaaaagaag 880
tgcatcgaaatcttctgcgtctacgtggtttctgcatgacaccaacagagcggcttcttg 1000
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On Dec
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Direct Submission
Submitted (02-NOY-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 98471)
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Liu,S.X., Lee,J.M., Sakano,H., Yu,G., Jhaveri,A., Lenz,C.,
Liu,S.X., Lee,J.M., Sakano,H., Yu,G., Jhaveri,A., Lenz,C.,
Toriumi,M., Chin,C., Chiou,J., Choi,E., Gonzalez,A., Howng,B.,
Toriumi,M., Chin,C., Chio,B., Altafi,H., Brooks,S.,
Koo,T., Li,J., Liu,A., Pham,P., Vaysberg,M., Altafi,H., Brooks,S.,
Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,M., Palm,C.,
Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Nguyen,M., Palm,C.,
Shinn,P., Tambunga,G., Davis,R.W., Ecker,J.R., Federspiel,N.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Arabidopsis thaliana
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Arabidopsis
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Dec 10, 1999 this sequence version replaced g1:6175131
Location/Qualifiers
1. 98471
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                                                                                                                                                                                                                                                                                                                                                     Conservative
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/db_xref-"taxon:3702"
/chromosome-"1"
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17757 c 17475 g 31738 t
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                                                                                                                                                                                                                                                                                                                                                                      21.8%;
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Pred. No. 1.6e-78;
0; Mismatches 274;
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RESULT AC006436 DEFINITION

complete sequence. ACOO6436 65899 bp Arabidopsis thaliana

chromosome II

section

N 17-DEC-1999 77 of 255 of the

tccaagataaacagcatataaa TCCAAGGTAAAAAAAAAAAAACA	ctcgacagataacttgcatgcttttgaattatctgg	1710 81058	B 8
CCTAA	GAGATTTTGAGGGAAGAGATTGATTTG	99	Db .
cgaacttctgaatggatcc	agtcatccatcaagacgtagaattagctcca	1650	ρ
aaagtgggacgagtggcaaaaa 3AAATGGGACGAATGGCAAAAA	ggtagtccgaatgcttgaaggtgatggccttgcagaa 	1590 80938	DP 6A
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cctaagatgt	aagtagcattactctgtacccagggtt	1530	Ş
Ĭ Ĭ Ĭ Ĭ Ĭ Ĭ GAGGAGAGAGACTGGAACAA	TAGTGGATCC	81	Db .
GATTGTTGAAGGAGAA ttgacacagaagttgac	TAATCTCAAATACTTGTTTGTTGGTTAGGI	80758	g g
gccttttgaaagagaaaaag	ttgttggatt	142	Qy
₽	ACTGGGTAATAACAACATAAAACTTCCATTTGACCCC	86908	ઠ
		1429	Qy
	CAGGACAAAGAGCTTTCGATCTCGCTCGGCTAGCTAAC	80638	Дb
gatgatgatgttat	tggacagagagettttgatettgetegeettge	1376	Qy
AATCATGCTTCTAGAACTAATC		57	당 :
ttatgctcttagago	aaqtcatcaqaqaagaccgatgtctttggttatgg	131	Ŷ
	ACGTGACAACAGCAGTCCGTGGCACCATCGGTCACATCG	51	당 .
ictcccaactacctctccac	rttagaactgetgtaagggtace	1256	9
		119	VQ.
GCAAACATCCTCTTAGACG	rgcgatccgaagatcattcaccgtgacgtaaa <i>a</i>	39	망
tgcaaatatattattggacgaa	tgatcccaagattatccatcgtgatgtaaaagc	1136	Qy
AGGTTTGTCTTACCTACATGA	CGGAAGAGAATCGCGCTAGGCTCAGCTC	80338	뭥
ggggctttcttatttgcatgac	gccaactaggaagaggattgcactaggatctgcta	1076	Ω
		27	g .
atcagaacctccccttgat	agcgtca	1044	γQ
TTTTCATGTTTTCCTTTATGGGT	CTTGTGCTCTCTCAATTACTTTGACGTGAAGTGTT	80218	망
		1044	γQ
TCTCA	TIGCTICGIG	80158	뭥
-#	tatccatacatggctaatggaagtgttgcgtcgtg	1001	Qy
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SOURCE
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                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and Netplantdene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, are named as 'unknown' proteins. Genes without sprinted as 'unknown' proteins or more gene prediction programs over most of their length are annotated as 'nypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wusll.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to the bottom of the chromosome.
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-DEC-1999) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA. On Dec 17. 1999 this sequence version replaced gi:4726109. The sequence and annotation of chromosome 2 were merged from those The individual closes on this chromosome after removing contains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC006436 AE002093
AC006436.4 GI:65
                                                                                                                                                                                                                                                                                                                                                                               F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                          This work was supported by the National Science Foundation, 
Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          overlaps. For detailed information, p
(http://www.tigr.org/tdb/at/at.html).
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                                                                                                                                                                                                                                                                                                                                                       database support.
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                                                                                                                                                                                            all correspondence to:
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/db_xref="taxon:3702"
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                                                                                                                                  .65899
                                                                                                                                                                 /Qualifiers
                                                                                                                                                                                         at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      please see the TIGR web site
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/gene="At2g13670"
<3349. .>5997
                                                                                                                           /pseudo 29450. .
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Apilryaaeieherprylylcryyafekahkldpsgggrgyrgfktllforlans

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ksekveavafeiiaaardvoekneiiapynilpldsagasgsymqleeykaavaalgu

Trglinnpsgfedhtkktgnldlddmlramfgfqaswllqaaqdiqqrkilymglytli

mgeaanirfwpeclcyifhnmayelhgllagnvsivtgenikpsyggddeaflrkvit
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join(3349. .3541.3644. .3744,4109. .4230,4375. .4471,
4583. .4693,4792. .4928,5629. .5755,5848. .5997)
//gene="Atzg13670"
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/gene="At2g13660"
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complement(join(451. .842,907. .1234))
/gene="At2g13660"
                    /rpt_family="POLY_A" complement(29932...30854) /gene="At2g13710"
                                                                                                                                                                                                                                                                                                                                                   TQEEEDDAVVVDSTPNLRSESFRAPKIEVTGSGLSEGYDARLSLKGRNGGGVLYLELS
LEVLAANSDVESGLIAEEKKGSSSSSLGLKNTCRIEVCDVERLGVERETVELMFEES
NVIIKKFMTMGVYRAIDVLEVAAGIKFSRAVLSCLKYLEAVPWTEDEEEKLRELLG
SFDDDAVSEILARFNSNETENLQDSLSKKLVWSITSCSDVNFRNELKSLVEKGLLCKSS
VYEKEQPEINKEDIYRAGKCCVDSLAKLFEEGSSSSSSKKEKPLIESISREVENINWL
LEIMIDREIAEEFVEIWGKQRRLVEMHERVSPMVRYEVSRVTGAIFIAMGKRRVQCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="At2g13690"
complement(<14929...>17114)
/gene="At2g13690"
/note="F13J11.4; predicted by genscan and genefinder"
complement(join(14929...15843,16401...17114))
/gene="At2g13690"
/note="hypothetical protein"
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SPPRNLYLCLRLYLLAFCHRSPEEIEQDEDSNSSYSVPINRINLINPPRRTDALNKPF
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/note="F137"
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WFSKHGTECPNLSKAFQIWWRRSFLRGVESSTCR"
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/db_xref="GI:4726112"
/translation="MGDSDLRRETNFGTGHLSRRRSWCCSFAVPPASPDTRSISSRNH
/translation="MGDSDLRRETNFGTGHLSRRRSWCCSFAVPPASPDTRTTMQETET
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/db_xref="GI:4726110"
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/note="F13J11.5"
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/note="F13J11.3"
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/db_xref="GI:4726111"
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                                                                                                      AAGTGTATAAAGGACGTTTAGCCGATGGCAATCTAGTGGCTGTCAAAAGGCTAAAAGAAG
                                                                                                                            aggtgtataagggacgccttgctgatggctcacttgtagcagttaaaaggcttaaagaag
                                                                                                                                                                       tgcaagtcgcaacggatacttttagtacca-----tacttggaagaggtggatttggta 820
tgcatcgaaatcttctgcgtctacgtggtttctgcatgacaccaacagagcggcttcttg
                                    AACGTACCAAGGGTGGGGAACTGCAGTTTCAAACCGAAGTTGAGATGATCAGTATGGCCG
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complement(<33782...>34228)
/gene="At231730"
complement(<33782...>34228)
/gene="At2313730"
/note="F13J11.8"
                                                                                                                                                                                                                                                                                                                                                                                  complement(37457...37522)
/rpt_family="(GAAAA)n"
join(<38993...39051,39561...
40095...40208)
/gene="At2g13750"
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AAEPRRTLGDENRPGMEYANRSAIVPPPYQRNDYESHLFYYITLHI"
complement(35689, .35776)
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QVMYSDFVTKKLKLYFTTSNQRKHININKKNYILKKNDKKSKKIILKKYEKKVIQYII
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complement(31832. .3
/rpt_family="(GAA)n"
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/gene="At2g13730"
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32232. .>33473
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/gene="At2g13720"
/note="F13J11.7"
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Pred. No. 2.6e-73;
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Sorghum bicolor Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyliophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.
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und Molekularbiologie der Pflanzen, Heinrich-Heine-Universitaet,
Universitaetstrasse 1, 40225 Duesseldorf, FRG
Location/Qualifiers
1, .2278
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SbRLKI, a receptor-like protein kinase of Sorghum bicolor Moench that is expressed in mesophyll cells Planta 208 (3), 420-425 (1999)

99312726
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/tissue_type="leaf"
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REIALGAARGLEYLHEBKONKILHRDVKAANVILDGNFEAVFORTV
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ttcaagtagcattactctgtacccagggttcgccaatggagcggcctaagatgtcagagg
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De, V.S., Schmidt, E.D., Van, H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
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                                                                                                                                          Direct Submission Submitted (06-MAY-1998) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laborator Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3934)
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Submitted (17-JUN-1999)
University, 4444 Forest
Submitted by:
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Sun,H., Wohldmann,P., Johnson,D. and
The sequence of A. thaliana F17123
Unpublished (1999)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Genome Sequencing Center
Department of Genetics, Washi
St. Louis, MO 63108, USA
e-mail: rwilson@watson.wustl
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MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing.

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone

NEIGHBORING COSMID INFORMATION

8 δÃ 밁 Qγ 밁 ğ 밁 QΥ BASE COUNT ORIGIN Ş 밁 밁 멼 FEATURES 밁 δÃ 밁 δ. Š 밁 Ş Query Match Best Local S Matches 460 46191 46131 CTTGGGAATCTAAGAAGCTTCACATTCAGAGAACTCCATGTTTATACAGATGGTTTCAGT 46431 46371 46311 TTTCGTATGGAGCTAGAGATGATTAGCTTAGCTGTTCATAAGAATCTGCTTCGGTTAATT 46251 1027 source 967 907 847 TCCAAGAACATTCTCGGCGCTGGTGGATTCGGTAATGTGTACAGAGGCAAGCTTGGAGAT ggtttctgcatgacaccaacagagcggcttcttgtatatccatacatggctaatggaagt 1026 tttcaaacagaggtggaaatgattagcatggctgtgcatcgaaatcttctgcgtctacgt 966 ----- eccatacttggaagaggtggatttggtaaggtgtataagggacgccttgctgat 846 aggctgttgtaggtgattttgggttagctaggctcatggattacaaggatacccatgtta ATCCCAAGATCATTCATAGAGATGTAAAGGCAGCTAATATTCTCTTAGACGAGTGCTTTG atcccaagattatccatcgtgatgtaaaagctgcaaatatattattggacgaagaatttg TGAGGAAGAGGATAGCAATTGGTGCAGCGAGAGGTTTGTTGTATCTACATGAGCAATGTG ctaggaagaggattgcactaggatctgctagggggctttcttattttgcatgaccattgtg 1141 GTCGCCTCTAAGCTTAAATGTTAGTATAATGTCTTGAACCATCAGTCCAAATCTCATTTT gttgcgtc-----GGTTATTGCGCAACTTCTGGTGAAAGGCTTCTTGTTTACCCTTACATGCCTAATGGAAGC 46430 GGGACAATGGTGGCAGTGAAACGGTTGAAGGATATTAATGGAACCTCAGGGGATTCACAG CGATGAGTTTTAACCAATTTTGTTTAACTGTTGTAGCTAAACCGGCATTGGACTGGAACA 46550 al Similarity 460; Conserv Actual end is 43094 Conservative start of this clone at 134784 of F17123. /organism="Arabidopsis t /cultivar="Columbia" /db_xref="taxon:3702" /clone="F17123" /chomosome="IV" /map="unknown" a 23410 c 23696 g 4458 Location/Qualifiers .134784 11.9%; gtgtttaagagagcgtcagccatcag------0, Score 216.2; DB 8; Pred. No. 2.2e-38; 0; Mismatches 238; ż base c -aacctccccttgattggccaa 1081 position Length 134784; Indels of. 71; F17I23; Gaps 1061 906 46190 46370 46250 1261 1201 46310 46490 46670 46610 actual ω

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Unpublished (1997)
2 (bases 1 to 120787)
2 (bases 1 to 120787)
Rederspiel,N.A., Davis,R.W., Conway,A.B., Palm,C.J., Conway,A.R., Kurtz,D.B., Buehler,B., Dewar,K., Feng,J., Kim,C., Li,Y., Shinn,P., Sun,H., Oji,O., Osborne,B., Shen,Y.K., Toriumi,M., Vyotskaia,V.,
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Submitted (09-JUL-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Federspiel, N.A., Davis, R.W., Conway, A.B., Palm, C.J., Conway, A.R., Kurtz, D.B., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Shinn, P., Sun, H., Oji, O., Osborne, B., Shen, Y.K., Toriumi, M., Vyotskaia, V., Yu, G., Theologis, A. and Ecker, J.
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Genomic sequence of Arabidopsis
                                                                                             Submitted (11-JUL-1997) Biochemistry, Sequencing and Technology Center, 855
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Au,M., Araujo,R., Brendel,V., Buehler,E., Dewar,K., Feng,J.,
Kim,C., Li,Y., Oji,O., Osborne,B.I., Shinn,P., Sun,H., Toriumi,M.,
Yyotskaia,V.,Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-JUN-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo
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Federspiel, N.A., Palm, C.
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Federspiel, N.A.,
                                                                                                                                                               Direct Submission
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   Palm, C.J.,
   Conway, A.B.,
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                                                                                         Stanford University/DNA California Avenue, Palo Alto
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Oji,O., Osborne,B.I., Shim,P., Sun,H., Toriumi,M.,
Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
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Jul 11, 19
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PFLFFDGESETSFFEDEEVEDRENSTHEYDATATKAYTQFKCLATMLQE*
Complement(3171. .4444)
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1845. .2159,2256. .2526,2788. .
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/translation="MGLSFAKLFSRLFAKKEMRILMVGLDAAGKTTILYKLKLGEIDE
LRDAVLLVFANKQDLPNAMNAAEITDKLGLHSLRQRHWYIQITCATTGEGLYEGLDWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(8347. .8443,8539.
/gene="F8A5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(8347. .9066)
/gene="F8A5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(3171. .3389,3471.
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/db_xref="taxon:3702"
                                                     /product="Phosphatidylinositol 3-kinase"
/protein_id="AAB71971.1"
/db_xref="GI:2462752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="nearly identical to
protein gp|D26537|537404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="F8A5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=
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| 77. .2876
                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F8A5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F8A5.2"
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                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                            /note="AtVps34"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start≠1
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.11164,11286.
.12395,12475.
.13572,13659.
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Vyotskaia,V.,
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VWDVSCGKTEGLIGGATVLLENSKMONKSGKOKLRLWOGKEADGSFPTSTPGKVPRHE
RGELERLEKLMNKYERGOIQSIDWLDRLMLKSLDTIKEGESTKEGSSHLFVVIDECSF
EHRVVFQESGANLFITAPIGSTNEFVTVWDTELGKTNESENKQLKARSLDRGIIDRD
LKPSNIERKSIGNELKYPPTRILSGDERGLLMFERESIMSGLKALKFERLKOVERSDVQ
EAKQAIQLMYKWEMIDVCDALELLSPLFESEVRAYAVSVLERADDEELQCYLLQLVQ
ALREERKSIGNEVGNALQNIELASFLRWYVAVELHDHVYAKRFYSTYELLEENI
IKLPGVNGEDGYQLWQSILVRQTELTAGLCSITREVRAVENTOKKIEKLRQLLGGLL
SELTYFEEPIRSPLTBWYLIKGIVAGESSLFKSALHPLALITFRTPEEGGSKKLIFKKG
DDLRQDQLVVQNWLMDRLLKLENLDLCLTPYKVLATGHDEGMLEFIPSRSLAQILSE
HRSITSYLQKFHEDEHAPFGITATCLDTFIKSCRGYSVITIRKSYCCEAXVILAKS
SNLILNLFHLMAGSTIPDIASDPEKGILKLQEKFRLDMDDEACIHFFQDLINESVSAL
FFQMVETIHRWAQYWR*
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//COUNTS CALL
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PILDY'UDRLRHLNVMRGGIHLPTIVVVGDQSGKSSVLESLAGISGPROGGICTRVPL
VMRLQRSSSEPEIMLESVNDKVYPTDEBHIABAIRAATDVIAGSGKGYSDAPLTHAVK
KAGVPDLTMVDLPGITRVPVNGQPENIYEQISGKNIMEYIEPQESIILNVLSATVDFTT
CESIRKSRKVDKTGQRTLAVVTKADMAPEGLLLQKVTADDVSIVLGYVCVRNRIGETIV
EEARMQEELLFRTHPVLSLIDEDIVGIPVLAVGLMILDTAGCLPKLVSKINGKLOETS
TAVLELNKLPMVMASTGEALMALMDIIGSAKESLLRILVGGDFSEYPDDQNMHCTARL
TAVLELNKLPMVMASTGEALMALMDIIGSAKESLLRILVGGDFSEYPDDQNMHCTARL
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join(15572. .16004,16236. .17812)
/gene="F8A5.5"
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RDGGGVEKMLEESPLVASKREKLQNSIKLLKESKDAVAAIVDQNC"
18712...22510
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DKPVEFINKIMDYIEDVLSSVTAKRSDNFPQIQSSIKRAGRNLISKIKEQSVNRVMEI
VEMEKLTDYTCNPEYMTSWTQKTSAQESFIDAVVKNENIPDYFSVTGFGNVKISHLRK
                                                                                                                                                                                                                                                       /translation="MGGSKMSNDYEIDVEAGMSSLSIVNTPIEAPIVSSYNDRIRPLL
DTVDRLRNLNYMREGICLPTIVVVGDQSGKSSVLESLAGINLERGQGICTRVPLVMR
LQRSSSPEPEIWLEYSDKVVPTDEEVAEATDVIAGTGBEVSDTPLTLSVKKN
VPDLPGITRVPVNGQPENIYEQISRMLMKYIEPQESIILLNYLSAFVDFTTCES
IRMSRQVDKTGERTLAVVTKADMAPEGLLQKVTADDVSIGLGYICVRNRIGEETYEEA
RVQEDLLFRTHELLSLIDGDIYGIL"
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/gene="F8A5.6"
/note="similar to "Mx" GTP-binding
/codon_start=1
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join(18712. .19150,19685. .1
21973. .22091,22335. .22510)
/gene="F8A5.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/protein_id="AAB71957.1"
/db_xref="GI:2462738"
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join(23787. .24210,24676. .
/gene="F8A5.7"
/note="similar to "Mx" GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYTPLTLHVKKADVPDLTLVDLPEITRVPVNGQTQNIHAKNLQGDYEVHQAT'
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/db_xref="GI:2462747"
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                                                                                                        complement(join(26476. .26936,27030. .28070,28540.
                                                                                                                                                          complement(26476. .28975)
/gene="F8A5.8"
11.9%;
Score 215.4;
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8;
Length 120787
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Matches 479; Conservative
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                                                                                                                                                                                                                                                                                                   cttttgatcttgctcgccttgcgaacgatgatgatgttatgtt 1430
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                                                                                                                                                                                                                                                                                                                                                                                                                               CAGTCCGTGGAACTGTTGGCCACATTGCACCTGAGTACTTATCCACGGGTCAGTCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ctgtaaggggtaccttgggctacatagctcccgagtacctctcgactggaaagtcatcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGTIGGIGATITIGGGITAGCITAGCCTICTAGACCATAGAGACTCTCATGTCACAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttgtaggtgattttgggttagctaggctcatggattacaaggatacccatgttacaactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTACATTTTTTGTTTAGATAATATCCGTGGAGAGCCAGCATTAGACTGGTCGAGAAGGA 108613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITTAGTCTACCCTTACATGCCAAATGGGAGTGTCGCATCACGCTTAAAAGGTAATGCAG 108733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ttcttgtatatccatacatggctaatggaagtgttgcgtcgtgtttaagagagcgtcagc 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCTCTTCATCGCAATCTCCTCCGGCTCCGCGGTTTCTGTAGTAGCAACCAGGAGAGAA 108793
                                                                                                                                                                                                                                                                                                                                                       AGAAGACTGATGTCTTTGGCTTTGGCATACTTCTCCTTGAGCTCATTACTGGTCAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGATTATACACCGCGATGTGAAAGCAGCTAACATTCTGTTAGATGAGGACTTCGAAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAAGATAGCGGTTGGGACAGCGAGAGGACTAGTTTACCTACACGAGCAATGTGACCCGA
Arabidopsis thaliana Eukaryota; Uridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                            complete sequence. AC005170 AE002093 AC005170.2 GI:659
                                                                                                                                                                  AC005170 110211 bp
Arabidopsis thaliana
                                                                                            HIG
                                                                         thale cress.
                                                                                                              GI:6598448
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                                                                                                                                                                      chromosome
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0; Mismatches 251;
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                                                                                                                                                                      II section
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135 of 255 of the
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                               gene
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                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prediction programs including GRAIL

(ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green,
University of Washington), Genscan (Chris Burge,
http://gnomic.stanford.edu/gENSCANW.html), and NetPlantGene
(http://www.cbs.dtu.dk/services/NetGene2/), searches of the
complete sequence against a peptide database and plant EST
databases at TIGR, and manual curations based on those analyses.
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are named
after the database hits. Genes without significant peptide
similarity but with EST similarity are named as 'unknown' proteins.
Genes without protein or EST similarity that are predicted by two
or more gene prediction programs over most of their length are
annotated as 'hypothetical' proteins. Genes encoding tRNAs are
predicted by tRNAscan-SE (Sean Eddy,
http://genome.washington.edu/RN/RepeatMasker.html). Genes are
numbered from the top to the bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis.

1 (bases I to 110211)

1 (bases I to 110211)

Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Ronning,C.M., Feldblyum,T.V., Buell,C.R., Ketchum, K.A., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,M.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-DEC-1999) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA. On Dec 17. 1999 this sequence version replaced gi:3738313. The sequence and annotation of chromosome 2 were merged from of the individual clones on this chromosome after removing of the individual clones on this chromosome after removing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lin,
                                                                                                                                                                                                                                                                                                                                                                                          Address all correspondence to:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jining Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bloinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This work was supported by the National Science Foundation, 
Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         database support.
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complement(356. .401)
/rpt_family="(TAA)n"
complement(join(1549. .2058,2731. .3012))
/gene="At2g23810"
complement(1549. .3012)
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/db_xref="taxon:3702"
/chromosome="2"
                                                                                                                                                                                                              complement(1. .2793)
                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                       at@tigr.org
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complement(3570. .3641)
/rpt_family="(TAAAA)n"
complement(4565. .4612)
/rpt_family="(CAA)n"
6379. .6484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(6654. .6712)
/rpt_family="(GAA)n"
join(<9531. .9582,9709. .9779,9866.</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mknunryffckslslvflypsftrshirftysaagasspuraih
cmasdspgscdgsvgspfnvaavpsssssssasaldflslctrlkgditspsglskes
kdprsladhdyrkdchallssddfbynrbkckmaatyhdlaeliveditspsglskes
knrresealehmckllgggerakeiaelwreyeensspeakvvkdfdkvellilgaley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(6480. .6749,7602. .
8152. .8268,8487. .8557)
/gene="nAt2g23820"
/note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="(CAAAA)n"
join(<6480. .6749,7602.
8152. .8268,8487. .8786)
/gene="at2g23820"
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complement(3567. .3677)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(1744. .2058,2731. .3003))
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TNRNNYCVTPMYGLILPKSTCKVLYTMQAQKEVPSDMQSFEKEMIQSVLASPGVTAKE
VTREMFSKESCHVVLETKLRVTYVCSTTINITSSPRIRRGFIFQCFC"
complement(11332...11371)
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IVFLVFLIIVYSVGCCAFRNNKRDDSYSRTYGYKP"
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   complement(join(20442. .20537,20617. .20691,20894. .20948,
21145. .21485))
                                                                                     complement(<20442. .>21485)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAC63657.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                          __family="(TAAA)n"
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Query Match
Best Local Similarity
Matches 467; Conserv
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                                      GACTTCTTGTTTACCCTTACATGTCCAATGGCAGCGTCGCCTCTAGGCTCAAAGGTAGTC
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/gene="At2g23850"
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/note="T29E15.8"
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CFRGLVLDISYRPVNVVCWKRAICLEYMDKADVLEYYDQTVSSPTGSFYIPAVLRVPH
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33162. .35713,35886. .>36147))
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Search completed: June 23, 2000, 23:41:42 Job time: 43857 sec

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20-N0V-1997, E02443,
13-MAY-1996; GB-010044.
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(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-086529/08.
P-PSDB; W47023.
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production of apomictic seeds - useful in plant breeding Claim 27; pages 91-95; 123pp; English. The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing
                                                                                                                                                                     03-AUG-1998 (first entry)
Arabidopsis thaliana SERK receptor kinase; apomixis; plant breeding; ds.
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Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
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aatcttctgcgtctacgtggtttctgcatgacaccaacagagcggcttcttgtatatcca
                              CCAGGTGGAGAGCTCCAGTTTCAAACAGAAGTAGAGATGATAAGTATGGCAGTTCATCGA
                                                 | ccaggtggtgagctgcagtttcaaacagaggtggaaatgattagcattggctgtgcatcga
                                                                                           GCGAGTGATGGGTTTAGTAACAAGAACATTTTGGGCAGAGGTGGGTTTGGGAAAGTCTAC
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                                                                                   carota
                                                                                                                                                standard;
                                                                                                                          (first entry)
                                                                                                                 SERK gene
                  /note= "cont
3731. .3802
/*tag= b
                                                              Location/Qualifiers 3696. .6620
                                                   /*tag=
                                                                                                                                                DNA;
                                                                                                                                                6695
                                      "contains
                                                                                                      apomictic;
                                                                                                                                                ВP
                                                                                                       seeds;
                                                                                                      production;
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Production of apomictic seeds - useful in plant breeding
Production of apomictic seeds - useful in plant breeding
Production of apomictic seeds
CC Claim 21; Pages 40-46; 123pp; English.
CC It may be used as part of a method of producing apomictic seeds
CC comprising: (a) transforming plant material with a nucleotide
CC comprising: (a) transforming plant material with a nucleotide
CC cell membrane renders the cell embryogenic; (b) regenerating
CC cell membrane renders the cell embryogenic; (b) regenerating
CC plant parts; and (c) expressing the sequence in the vicinity
CC plant parts; and (c) expressing the sequence in the vicinity
CC plant parts; and (c) expressing the sequence in the vicinity
CC can be developed into plant progeny. This is useful in plant
CC can be developed into plant progeny. This is useful in plant
CC can be developed into plant improvement and cultivar development in
CC the case that sexual plants are available as crosses with the
CC apomictic plant. Apomixis provides for true-breeding, seed
CC propagated hybrids and could shorten and simplify the breeding
CC process so that selfing and progeny testing to produce and/or
CC specific stable traits for such characteristics as height,
CC seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
                                                                                                                                                                                                       Query Match 30.9
Best Local Similarity 81.9
Matches 735; Conservative
                                                                                                                                                                             1044
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20-NOV-1997: E02443.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG, Schmidt EDL, Van Holst WPI; 98-086529/08.
P-PSDB; W47013.
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/nnumber= 2
4124. .4211
/*tag= d
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/number= 5
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/number= 8
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/*tag= h
/number= 7
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/*tag= g
/number= 6
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                                                                                                                                                                                                       Score 560.2; DB Pred. No. 8e-134; D; Mismatches 1
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                                                                                                                                                                                                                                 Length 6695
                                                                                                                                                                                                         Indels
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gttaaaagccttttgaaagagaaaaagttggagatgctggtcgatcctgacctggagaac
                                                                                                                                                                                                                                                                               | 9990tacatagctcccgagtacctctcgactggaaagtcatcagagaaagaccgatgtctt
                                                                            TGGGCACATAGCTCCCGAGTACCTCTCGACTGGAAAGTCATCAGAGAAGACCGATGTCTT
                                          ccacatcgaacttctgaatggatcctagactcgacagataacttgcatgcttttgaatta 1740
                                                                                                                                                                                                            TGCCTGTATTTGATTCTTAGTCATGTTATGCATATTGACCTGCTTTGCAATGTCTTTTAG
                                                                                                                                                                                                                                             GGTTAATTATTTCACATATTAGTGCTTACTACTTTGTTGTGGCCCCTTTGTTTTATTTCC 6279
                                   CCACATCGAACTTCTGAATGGATCCTAGACTCGACAGATAACTTGCATGCTTTTGAATTA
                                                                    GTTAAAAGCCTTTTGAAAGAGAAAAAGTTGGAGATGCTGGTCGATCCTGACCTGCAGAAC
                  1797
 6695
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VYOSSE VOCAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V06585;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK gene.
receptor kinase; apomixis; apomictic; seeds; production; embryos;
plant breeding; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis
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/number 4
4430. .4528
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/number= 2
4124 .4211
/*tag= d
/number= 3
4284 .4357
/*tag= e
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3731. .3802
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Claim 26; Pages 64-67; 123pp; English.

It may be used as part of a method of producing apomictic seeds comprising; (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryos ac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed apomixis allows plant breeders to develop cultivars with special stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 504
 3602
                                                                                                     3482
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                                                                                                                                                                                                                                                          3302
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                                                                                                                            881
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                                                                                                                                                                                                                                                         CAGCCGAAGAAGATCCAGAAGTTCATCTGGGACAGCTCAAGAGGTTTTCTTTGCGGGAGC 336
                                                                                                                                                                                                                                                                      tatatccatacatggctaatggaagtgttgcgtcgtgtttaag------
                                                                                                                 aacgaacaccaggtggtgagctgcagtttcaaacagaggtggaaatgattagcatggctg
                                                                                                                                                                    aggtgtataagggacgccttgctgatggctcacttgtagcagttaaaaggcttaaagaag
                                                                                                                                                                                                                      tgcaagtcgcaacggatacttttagt-----accatacttggaagaggtggatttggta
                                                             tgcatcgaaatcttctgcgtctacgtggtttctgcatgacaccaacagagcggcttcttg
                                                                                                                                                                                                       TACAAGTGGCGAGTGATGGGTTTAGTAACAAGAACATTTTGGGCAGAGGTGGGTTTGGGA
                                                                                                   AGCGAACTCCAGGTGGAGAGCTCCAGTTTCAAACAGAAGTAGAATGATAAGTATGGCAG
                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                             Conservative
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/*tag= i
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                                                                                                                                                                                                                                                                                                                        14.98;
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                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                        Score 270.8;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                           Indels 119;
                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                     4081;
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                               880
                                                                                                  3541
                                                                                                                            940
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2772 CAGTAAAGCGACTIGCTGTAGGACGTTTTCAGGGGGATT---CAACAGTTTGATGCAGAAA 2828

cagttaaaacgcttaaagaagaacgaacaccaggtggtgagctgcagtttcaaacagagg TAGGCAGTGGAGGTTTTGGAGCAACATACAAAGCGGAGATTGCACCAGGGTTCCTAGTGG

2712

800 ttggaagagstggatttggtaaggtgtataagggacgccttgctgatggctcacttgtag

Query Match Best Local S Matches 350

Similarity

7.9%;

Score 143.4; DB 1; Pred. No. 3.2e-27; 0; Mismatches 296;

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Length

3842;

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Gaps

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Conservative

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Case be used for tomato.
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                                                                                            generating transgenic plants resistant to Xanthomonas Claim 14; Page 61-62; 67pp; English.
This invention describes a method for conferring disease resists plants. The invention describes the use of novel genes and prote belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and protesses are the control of th
                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1999. U14841. 17-JUL-1998; U14841. 13-JUG-1997; US-910386. 13-JUG-1997; US-910386. (REGC ) UNIV CALIFORNIA. Hulbert SH, Richter T, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUN-1999 (first entry)
Tomato Xa21 clone TRK2 DNA fragment.
Ya21; receptor kinase-like protein; multic
plant disease resistance; cassava; maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3902
                                                                                                                                                                                                                                                            New RRK polynucleotides and nucleic acid ogenerating transgenic plants resistant to
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X23533;
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1; 99-204431/17.
PSDB; W23533.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcatgaccattgtgatcccaagattatccatcgtgatgtaaaagctgcaaaatattatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAACCGGAAAATCTTCAGAGAAAACCGACGTTTTCGGATACGGAATCATGCTTCTAGA
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         New receptor kinase Bin1 involved in brassinolide signalling useful for promoting increased yield and disease resistance in plants and for modulating occyte maturation plants and for modulating occyte maturation the plants and for modulating occyte maturation the plants of the plant steroid receptor kinase, the synthesis of the plant steroid hormone, brassinolide. 18 New Arabidopsis dwarf mutants were identified that lacked the ability to respond to brassinolide, and were named bin mutants. The bin1 mutations were used to map the gene to a small interval on Arabidopsis chromosome 4. Bin1 was choned by map-based cloning. The Bin1 polynucleotide was identified within this interval by sequencing the wild-type and mutant alleles of this nucleic acid. Overexpression of Bin1 in transgenic plants provides plants
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30-DEC-1998.
24-JUN-1998; U13100.
24-JUN-1997; US-881706.
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WPI; 99-081275/07.
P-PSDB; W97819.
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Best Local Similarity 53.6
Matches 343; Conservative
x23531 standard; cDNA; 3045 BP.
x23531;
17-JUN-1999 (first entry)
Maize Xa21 gene DT4 cDNA fragment.
xa21; receptor kinase-like protein;
plant disease resistance; cassava; n
Zea mays.
W09909151-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant yield or vegetative biomass and increased seed yield. Expression of Bini may also increase resistance to pesticides. Inhibition of Bini may also increase resistance to pesticides. Inhibition of Bini, e.g. using antisense oligonucleotides (AON), is used to render plants male sterile, and to reduce their stature or yield, e.g. for creating dwarf varieties. Since Bini homologues may be involved in regulation of the menstrual cycle and uterine function, Bini, antibodies and AON may be useful as contraceptives, for improving success of in vitro fertilisation and to prevent premature labour. Transgenic animals are also provided, and are models for studying steroid-receptor interactions or can be used to screen for therapeutic agents.
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                                   e protein; multigene family; cassava; maize; tomato; Xant
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17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ro
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This invention describes a method for conferring disease resistance in plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes and proteins canssava, maize and tomato are also described. The genes and proteins can be used for enhancing resistance to Xanthomonas in a plant, preferably in
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Sequence 3045 BP;
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Pred. No. 6.6e-27;
D; Mismatches 281
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CDNA clones TRKI (T31307) and TRLI (T31308) were isolated from the conversation of tomato cDNA using primers (T31301-06) based on the crice disease resistance Xa21 gene (T31300). They belong to the RRK CC family of disease resistance genes. TRKI (tomato receptor kinase 1) is present as 1 or 2 copies in the tomato genome and 1 copy maps to the short arm of chromosome 1 in the proximity of a resistance gene to Xanthomonas campestris by vesicatoria RXI. It encodes an RKK CC transduction pathways leading to a defence response. The gene is cuseful for engineering disease resistance in tomato and other plants. SQ Sequence 1554 BP; 477 A; 303 C; 348 G; 426 T;
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Matches 423
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07-JUN-1995; US-475891.
29-SEP-1995; US-004645.
(REGC) UNIV CALIFORNIA.
Ronald PC, Song W, Szab
WPI; 96-354532/35.
P-PSDB; W03186.
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Tomato RRK gene clone TRK1.
Xa21; RRK; disease resistance; Xanthomonas; blight; rice;
tomato receptor kinase 1; TRK1; transgenic plant; crop protection;
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                  gtaaggggtaccttgggctacatagctcccgagtacctctcgactggaaagtcatcagag
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17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New RRK polynucleotides and nucleic acid constructs - used for generating transgenic plants resistant to Xanthomonas Claim 14, Page 59-60, 67pp, English.
This invention describes a method for conferring disease resistance plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and protein
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Xa21; receptor kinase-like protein; multi-
plant disease resistance; cassava; maize;
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                       DNA encoding plant morphogenesis regulatory protein - useful yield plants with short stems or altered inflorescence claim 1; Pages 6-10; 17pp; Japanese.
The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to a plant with, e.g. short stems or altered inflorescence. The acts on a plant at a specific site for a specific period, and therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform plant to increase its MRP expression, and therefore control the plant to increase its MRP expression, and therefore control to the plant to increase its MRP expression, and therefore control to the plant to increase its MRP expression.
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(MITS-) MITSUI GYOSAI SHOKUBUTSU (CHIK') ZH CHIKYU KANKYO SANGYO G WPI; 97-206629/19.
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lation; short; stem; alteration
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Query Match
Best Local Sin
Matches 321;
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26-SEP-1996; 254945.
26-SEP-1996; JP-254945.
(SAIS-) SAISHU JITSUYO G
WPI; 98-289869/26.
P-PSDB; W56307.
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23-JUL-1998 (first entry)
Clas I S-receptor kinase (SRK) g
Class I S-receptor kinase; SRK;
                                                                                       S-locus glycoprotein gene - and S receptor kinase gene of c
type and class II type to produce recombinant plants
Disclosure; Fig 2; 20pp; Japanese.
The present sequence represents a class I S-receptor kinase
gene. The sequence was isolated from Brassica camestris S45
Sequence 2640 BP; 800 A; 491 C; 645 G; 704 T;
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 Pred. No. 1.30
0; Mismatches
                 Score 121.2;
Pred. No. 1.
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.6e-26;
.es 211;
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l.3e-21;
les 268;
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EP-519869-A.
23-DEC-1992; 810449.
10-JUN-1992; 810449.
19-JUN-1991; US-717331.
(CIBA) CIBA GEIGY AG.
Nasrallah ME, Stein J
WPI; 92-426051/52.
P-PSDB; R29814.
New Brassica gene for S-receptor ki
incompatibility to plants - has ext
to S-locus glyco-protein gene
Claim 8; Page 51-52; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  S receptor kinase gene SRK6.

S-receptor; kinase; SRK; pistil; anther; stigmatic; self-incompatibility; primary; transmitter; pollen 1 signal; S-locus; binding domain; transmembrane; prof glycoprotein; SLG; SRK6; SRK2; ZMPK1; ss.
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Q32648;
Q4-MAY-1993 (first entry)
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Best Local S
Matches 317
                                                          T13443;
10-10Wn-1996 (first encry,
SRK-A10 cDNA.
S locus receptor kinase; SRK-A10; S
self-incompatibility; hybrid seed;
canola; oilseed; vector; ds.
canola; oilseed; vector; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences given in 032648-49 represent two S-receptor kinase (SRK) genes. These genes are transcribed specifically in pistils and anthers and are involved in the stigmatic self-incompatibility (SI) response of Brassica. The protein products of these genes are thought to be the primary transmitters of the pollen recognition signal in the SI response. The SRK proteins comprise an S-locus binding domain, a transmembrane domain and a protein kinase domain. The S-locus binding domain is pref. substantially homologous to an S-locus glycoprotein (SIG) gene. The kinase domain has a degree of homology with the kinase domain of SRK6, SRK2, and ZMPKI.
                                              Brassica
Key
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Pred. No. 4.1e-20;
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12-SEP-1995.
17-MAY-1994; 123751.
11-MAX-1994; US-208909.
11-MAY-1994; US-242104.
(ROTH/) ROTHSTEIN S J.
GLAVIN TL. GOZING DR, I
WEI; 96-180298/19.
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CDNA clone SRK-A10 (T13425) codes for an S locus receptor kinase associated with the A10 self-incompatability allele of Brassica napus. It was isolated from genomic DNA of rapeseed line W1 by PCR amplification. The gene contains a 1 bp deletion resulting in premature termination of translation and prodn. of truncated SRK-A10 protein. Expression vectors contg. a corrected SRK-A10 gene (see T13423) are used to produce self-incompatible plants able to produce hybrid seed in improved yields.

Sequence 2685 BP; 816 A; 512 C; 639 G; 718 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAATGAGGTGACATTAATCGCGAGGCTTCAACATGTAAATCTTGTGCAAATTCTTGGCTG 1800
                   gaagaccgatgtctttggttatgggattatgctcttagagctcattactggacagaga
                                                                                                                                                                                                                             tatccatcgtgatgtaaaagctgcaaatatattattggacgaagaatttgaggctgttgt
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                                                                              tgtaaggggtaccttgggctacatagctcccgagtacctctcgactggaaagtcatcaga 1328
                                                                                                                                                     CATTACCAATGGTGTTGCTCGAGGGCTTTTATATCTTCATCAAGACTCCCGCTTTAGGAT
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                                                                Conservative
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Pred. No. 5.7e
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RESULT T13423

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Query Match
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Matches 317; Conser
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12-SEP-1995.
17-MAY-1994; 123751.
11-MAR-1994; US-208909.
11-MAY-1994; US-242104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yield (Claim 8; Fig 3; 39pp; English. Claim 94 Self-incompatability allele of Brassica napus. The gene contains a 1 bp deletion resulting in premature termination of translation and prodn. of truncated SRX-Al0 protein. A 'corrected' gene (T13423) has a, c or g inserted at position 948 (T13423). Incorporation of the corrected gene into an expression vector allows the breeding of self-incompatible plants able to produce hybrid seed in improved yields. Sequence 2686 BP; 816 A; 513 C; 638 G; 718 T;
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T13423;
10-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRK-A10 gene mutant N948.
S locus receptor kinase; SRK-A10; self-incompatibility; hybrid seed;
                                                                                                                                                     1152
                                                                                                                                                                                                                                                                                                                                                                                                                   1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA mols. encoding S locus glycoprotein or receptor kinase - expression vectors contg. the DNA can be used to produce expression plants, which ensure hybrid progeny and increase in the compatible plants, which ensure hybrid progeny and increase
       1269
                                                                                                                    1979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 canola; oilseed; vector; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ROTH/) ROTHSTEIN S J. Glavin TL, Goring DR, WPI; 96-180298/19.
                                                                                                                                                                                                                                                                                                                                                                             972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            792
                                                                                                                                                                                                                                                                                       gtcgtgtttaagagagcgtcagccatcagaacctccccttgattggccaactaggaagag
                                                                                                                                                                                                                                                                                                                                                                 ctgcatgacaccaacagagcgcttcttgtatatccatacatggctaatggaagtgttgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  taccatacttggaagaggtggatttggtaaggtgtataagggacgccttgctgatggctc
                                                                                                                                                                                      CATTACCAATGGTGTTGCTCGAGGGCTTTTATATCTTCATCAAGACTCCCCCTTTAGGAT
                                                                                                                                                                                                               gattgcactaggatctgctagggggctttcttatttgcatgaccattgtgatcccaagat 1151
                                                                                                                                                                                                                                                                                                                                                                                                               GAATGAGGTGACATTAATCGCGAGGCTTCAACATGTAAATCTTGTGCAAATTCTTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                     aacagaggtggaaatgattagcatggctgtgcatcgaaatcttctgcgtctacgtggttt 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAACAAAATTGGACAAGGTGGTTTTGGTATTGTTTACAAGGGGATATTACTTGACGGGCA
tgtaaggggtaccttgggctacatagctcccgagtacctctcgactggaaagtcatcaga
                                                                aggtgattttgggttagctaggctcatggattaccaaggatacccatgtt---acaactgc
                                                                                                              AATCCACAGAGATTTGAAAGTAAGTAACATTTTGCTTGATAGAAATATGGTCCCAAAGAT
                                                                                                                                     tatccatcgtgatgtaaaagctgcaaatatattattggacgaagaatttgaggctgttgt
                                                                                                                                                                                                                                                                                                                                        TTGCATTGACGCAGATGAGAAGATGCTGATATATGAGTATTTGGAAAATTTAAGCCTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAAATCGCGGTAAAAAGGCTATCAAAGACGTCAGTTCAAGGGGGTTGATG---AGTTTAT 1741
                                      CTCGGATTTTGGAATGGCCAGGATATTTGAAAGAGACGAGACGGAAGCTAACACAATGAA
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948
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/note= "a, c or g may
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53.0%;
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Pred. No. 5.7e
0; Mismatches
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transgenic plant; rapeseed;
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5.7e-20;
nes 272;
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Plant; morphogenesis; regulation;
inflorescence; extraneous; gene;
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lation; short;
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ph 04-MAR-1997; 216187.

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Search completed: June Job time: 40366 sec 23, 2000, 22:49:30

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Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 14, Appl	Sequence 27, Appl	Sequence 22, Appl	Sequence 1, Appli	Sequence 1, Appli	•	Sequence 51, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 7, Appli

ALIGNMENTS

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Sequence 24, Application US/08587680A
Patent No. 5977434

GENERAL INFORMATION:
APPLICANT: Wang, Guo-Liang
APPLICANT: Scab, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
APPLICANT: Scab, Veronique
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: Galifornia
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Insh PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION NUMBER: US 08/475,891
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,375
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,375
FILING DATE: 29-SEP-1995
PRIOR APPLICATION NUMBER: US 08/567,375
FILING DATE: 104-DEC-1995
ATTORNEY/ACENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
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RESULT 2
US-07-717-331F-9
; Sequence 9, Application US/07717331F
; Patent No. 5484905
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA (partial)
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ilarity 51.8%;
Conservative
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pred. No. 4.2e-29;
0; Mismatches 375
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Best Local S
Matches 318
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CURRENT APPLICATION.

APPLICATION NUMBER: US/07//1/,

APPLICATION June 19th 1991

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: George M. Yahwak

REGISTRATION NUMBER: 26,824

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203)268-1951

TELEFAX: (203)268-1951

TELEFAX: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: June Nasrallah; michael Nasrallah; and APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At The Self-Incompatal
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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CITY: Trumbul
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                                                                                                                                          ttatccatcgtgatgtaaaagctgcaaatatattattggacgaagaatttgaggctgttg 1210
                                                                                                                                                                                                                                                                                                                                                               totgoatgacaccaaccagagoggottottgtatatccatacatggotaatggaagtgttg 1030
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                                                                                                                                                                                                                  ACATTACCAATGGTGTTGCTCGAGGGCTTTTATATCTTCATCAAGACTCACGGTTTAGGA 1945
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TCTCGGATTTTGGGATGGCCAGGATATTTGAAAGGGACGAAACGGAAGCTAACACAATGA
                                  taggtgattttgggttagctaggctcatggattacaaggatacccatgtt---acaactg 1267
                                                                                                       TAATCCACAGAGATTTGAAAGTAAGTAACATTTTGCTTGACAAAAATATGATCCCAAAGA
                                                                                                                                                                                                                                                                      ggattgcactaggatctgctagggggctttcttatttgcatgaccattgtgatcccaaga 1150
                                                                                                                                                                                                                                                                                                                               ATTCTTATCTCTTTG---GTAAAACCCGAAGGTCTAAGCTAAATTGGAATGAGAGATTCG 1885
                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTGCATTGAAGGAGATGAGAAGATGTTGATATATGAGTATTTGGAAAATTTAAGCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAATGAGGTGACACTAATTGCGAGGCTTCAGCATATAAACCTTGTTCAAGTTCTTGGCT 1768
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25 Skytop Drive
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nilarity 53.3%;
Conservative
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Encoded At The Self-Incompatability Locus
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US-07-717-331F-1
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Best Local Similarity
Matches 318; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
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1031 cgtcgtgtttaagagagcgtcagccatcagaacctccccttgattggccaactaggaaga 1090
                                                                                                                                                                                                        1652 AAGAAATTGCAGTAAAAAGGCTATCAAAGACGTCAGTTCAAGGGACTGATG---AGTTTA 1708
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                                                                                                                                                                                                                                                                                  1592 GTAACAAACTCGGACAAGGTGGTTTTGGTATTGTTTACAAGGGAAGATTACTTGACGGGA 1651
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                                                                                                                                                       911 aaacagaggtggaaatgattagcatggctgtgcatcgaaatcttctgcgtctacgtggtt 970
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CITY: Trumbull
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FILING DATE: June 19th 1991
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
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                                                        GTTGCATTGAAGGAGATGAGAAGATGTTGATATATGAGTATTTGGAAAATTTAAGCCTTG
                                                                                          tctgcatgacaccaacagagcggcttcttgtatatccatacatggctaatggaagtgttg
                                                                                                                               TGAATGAGGTGACACTAATTGCGAGGCTTCAGCATATAAACCTTGTTCAAGTTCTTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2833 base pairs
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(203)268-1951
(203)268-1951
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Encoded At The Self-Incompatability Locus
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                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                             270;
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US-08-265-628-1
                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:

NAME: POCHOPIEN Ph.D., Donald
REGISTRATION NUMBER: 32,167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
TELEPHAX: 312-707-9155
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08265628 Patent No. 5821094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Rothst
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CITY: Chicago
THATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1091 ggattgcactaggatctgctagggggctttcttatttgcatgaccattgtgatcccaaga 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Goring, Daphne TITLE OF INVENTION: S-LOCUTION: SELF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1268 ctgtaaggggtaccttgggctacatagctcccgagtacctctcgactggaaagtcatcag 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1886 ACATTACCAATGGTGTTGCTCGAGGGCTTTTATATCTTCATCAAGACTCACGGTTTAGGA 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1829 ATTCTTATCTCTTTG----GTAAAACCCGAAGGTCTAAGCTAAATTGGAATGAGAGATTCG 1885
                                                        HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                           LENGTH: 2745 ....
TENGTH: 2745 ....
TYPE: nucleic acid
sing
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
APPLICATION NUMBER:
FILING DATE: 03-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  STRAIN: O. INDIVIDUAL
                                                                                                                                       TOPOLOGY:
                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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RESULT 5
US-08-447-185-2
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Best Local Similarity
                                                                                                                                                                         Sequence 2, Application US/08447185 Patent No. 5648599
GENERAL INFORMATION:
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                                                              APPLICANT: Tanksley, Steven D.
APPLICANT: Martin, Gregory B.
TITLE OF INVENTION: GENE CONFERRING DISEASE
TITLE OF INVENTION: TO PLANTS BY RESPONDING
NUMBER OF SEQUENCES: 5
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                            1326 agagaagaccgatgtctttggttatgggattatgctctttagagctcattactggacagag 1385
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CHROMOSOME/SEGMENT:
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AUTHORS: ROTHSTEIN, STEVEN J.
TITLE: THE S-LOCUS RECEPTOR KINASE GENE IN A
TITLE: SELE-INCOMPATIBLE BRASSICA NAPUS LINE
TITLE: FUNCTIONAL SERINE/THREONINE KINASE
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO
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Best Local Similarity
Matches 340; Conserv
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INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Goldman Mr., Michael TELECOMMUNICATION INFORMATION: TELEPHONE: (716)263-1000
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MEDIUM TYPE: Floppy disk
                       1283
                                                                                                                                                                                                                                                                                         1106
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STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                               CAGCCAGAGGTC-----TACACTACCTTCATACTAGAGCAATTATACATCGTGATG
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tgggctacatagctcccgagtacctctcgactggaaagtcatcagagaaagaccgatgtct 1342
                                                                                                                                                      TCAAGTCTATAAACATATTGCTTGATGAGAATTTTGTGCCAAAAATTACTGATTTTGGAA
                                                                                                                                                                           taaaagctgcaaatatattattggacgaagaatttgaggctgttgtaggtgattttgggt 1225
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                                                                   TATCCAAGAAAGGGACTGAGCTTGATCAAACCCATCTTAGCACAGTAGTGAAAGGAACTC
                                                                                            tagctaggctcatggattacaaggat---acccatgttacaactgctgtaaggggtacct 1282
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Pred. No. 4.1e-18;
0; Mismatches 299;
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Length Indels

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RESULT 6
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Goldman Mr., Michael L. TELECOMMUNICATION INFORMATION: TELEPHONE: (716)263-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tanksley, Steven D.
APPLICANT: Martin, Gregory B.
TITLE OF INVENTION: GENE CONFERRING DISEASE RESISTANCE
TITLE OF INVENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PATHOGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1343 ttggttatgggattatgctcttagagctcattactggacagagagcttttgatcttgctc 1402
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                 806
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                                                                                                                                                                         866
                                                                                                                                                                                                              209
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986 cagagoggottottgtatatocatacatggotaatggaagtgttgogtcgtgtttaagag 1045
                                                          326
                                                                                                                                     269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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                                                                                                                                                                                                                                  gaggtggatttggtaaggtgtataagggacgccttgctgatggctcacttgtagcagtta 865
                                                          CTCTCTCATTTTGCAGACATCCGCATCTGGTTTCATTGATAGGATTCTGTGATGAAAGAA 385
                                                                                                                                                                                                          ATGGTGTCTTTGGGAAGGTTTACAAGGGTGTTTTGCGTGATGGAGCAAAGGTGGCCCTGA
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                                                                                            tgattagcatggctgtgcatcgaaatcttctgcgtctacgtggtttctgcatgacaccaa 985
                                                                                                                                 AAAGGCGTACACCTGAGTCCTCACAAGGTATTGAAG---AGTTCGAAACAGAAATTGAGA
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Pred. No. 6.7e-18;
0; Mismatches 299;
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US-07-717-331F-4
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                                                                                                                  US-07
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2749 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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GENERAL INFORMATION:
                 Query Match
Best Local Similarity
Matches 305; Conserv
                                                                                                              TOPOLOGY: 11
MOLECULE TYPE:
7-717-331F-4
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/7
FILING DATE: June 19th 1991
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: GEOTGE M. Vahwak
REGISTRATION UMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
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TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At The Self-Incompatability
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                                                                                                                                                                                                                                           : (203)268-1951
(203)268-1951
TO NO: 4:
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                     Conservative
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50.5%;
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                     0
                 Score 92; DB 1;
Pred. No. 8.7e-16;
0; Mismatches 29(
                                                     Length 2749
                   9;
                   Gaps
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RESULT 8
US-08-473-553A-1
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                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Prote
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
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                                                         US/08/473,553A
                                                                                                  Version
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Suite 3400
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; NAME/KEY:
; LOCATION:
US-08-473-553A-1
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REGISTRATION NUMBER: 38,304
REFERENCE_DOCKET NUMBER: A-60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 232; Conserv
                                                                                                                                                                              sequence 3, Application Patent No. 5952485 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pair
         APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Llang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                              4948
                                                                                                                                                                                                                                                                                                                                                                                                                                     4888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4594 GACGTCGCGATTAAACGACTCGTTGGCCGTGGGACCGGGAGGAGCGATCATGGATTCACG 4653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4534 AACATAATCGGTAAAGGCGGCAGTGGAATTGTCTACCGTGGATCAATGCCAAACAACGTA 4593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
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CORRESPONDENCE ADDRESS:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acagaggtggaaatgattagcatggctgtgcatcgaaatcttctgcgtcttacgtggtttc 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cttgtagcagttaaaaggcttaaagaagaacgaaccaggtggtgagctgcagtttcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atccatcgtgatgtaaaagctgcaaatatattattggacgaagaatttgaggctgttgta 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGCTTTT-----GCATGGATCTAAAGGTGGTCATCTTCAATGGGAGACGAGACATAGA 4827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAGCGAACAAGGATACGAATCTCCTTCTTTATGAGTACATGCCTAATGGAAGCCTTGGA 4773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgcatgacaccaacagagcggcttcttgtatatatccatacatggctaatggaagtgtttgcg 1032
                                                                                                                                                                                                                                                                                                                                              GCTGATTTTGGGCTTGCTAAGTTCTTAGTTGA 4979
                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGCATAGAGATGTTAAGTCCAATAACATTCTTTTGGACTCTGATTTTGAAGCCCATGTT 4947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAGCCGTGGAAGCTGCAAAGGGCTTGTGTTATCTTCACCATGATTGTTCACCATTGATC
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5117..5467
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2434..5037
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51.3%;
                                                                                                                                                                                                                            US/08567375
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Pred. No. 2.1e-14;
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                                                                 Conferring
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US-08-567-375-3
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Best Local Similarity
Matches 172; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
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PRIOR APPLICATION NUMBER: US 60/004,645
                                                                                1364
                                                                                                                                                                 1304
                                                                                                                                                                                                                                               1244
                                                                                                                                                                                                                                                                                                                                                                                                                  1126 ACTTCGCTTAGTTTTCTTGCACTTGAATTGAATAAGATCACAGGAAGCATTCCGAAGGAT 1185
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                                                                                                                                                                                                                                                                                                                                  1186 ATTGGCAATCTTATTGGCTTACAACATC--TCTATCTCTGCAACAACAATTTCAGAGGGT 1243
                                                                                                                                                                                                                                                                                                                                                                         146
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1424 TGTCATTAGGCCTTTCAACTAATAACCTTAGTGGTCCAATACC 1466
                                                                                                                                                                                                      266
                                                                                                                                                                                                                                                                         206 caattcctagtgatcttgggaatctgacaaatttggtgagcttggacctatacatgaata
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STREET: Tw
CITY: San
                                                                                                                                                                                                                                                                                                                                                                                                                                          86 aattotatatgaatogtaacagtataaatatattaaattacatgcagttoactgatgctt 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product= "Xa-21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/01 FILING DATE: 04-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0.
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                aagtootggatttatcaaacaatoggotatoaggaccagtacc 428
                                                                                                                                                                                           gcttctctggacctataccggacacattaggaaagcttacaaggctaagattcttgcgtc 325
                                                                                                                                                                                                                                               CTCTTCCATCATCGTTGGGCAGGCTTAAAAACTTAGGCATTCTACTCGCCTACGAAAACA 1303
                                                                                                                                                                                                                                                                                                                                                                accttgacaaatatggggttcttatgacattggagctttacagcaataacataagtggac 205
                                                                                                      tcaacaacagcotototggtccaattccaatgtcaotgactaatattacaactottc 385
                                                                                                                                                              ACTTGAGCGGTTCGATCCCGTTGGCCATAGGAAATCTTACTGAACTTAATATCTTACTGC 1363
                                                                            TCGGCACCAACAATTCAGTGGTTGGATACCATACACACTCTCAAAACCTCACAAACTTGT 1423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3921 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 1.6e-06;
0; Mismatches 169;
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, NAME/KEY: CDS
; LOCATION: join(1..2676, 3520..3918)
; OTHER INFORMATION: /product= "Xa-21"
US-08-587-680A-3
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US-08-587-680A-3
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                                                                                                                                                   Query Match 3.2%;
Best Local Similarity 50.1%;
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: Ronald.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
1186 ATTGGCAATCTTATTGGCTTACAACATC - - TCTATCTCTGCAACAACAATTTCAGAGGGT 1243
                                                                          1126 ACTTCGCTTAGTTTTCTTGCACTTGAATTGAATAAGATCACAGGAAGCATTCCGAAGGAT 1185
                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                      146 accttgacaaatatggggttcttatgacattggagctttacagcaataacataagtggac 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two .....
CITY: San Francisco
                                                                                                86 aattotatatgaatogtaacagtataaatatataaattacatgcagttcactgatgctt 145
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bastian, Kevin REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08 FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/01 FILING DATE: 17-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                       3921 base pairs
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Song, Wen-Yuang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Szabo, Veronique
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                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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                                                                                                                                                   Score 58.6; DB 4;
Pred. No. 1.6e-06;
0; Mismatches 169
                                                                                                                                                                                           DB 4;
                                                                                                                                                       169;
                                                                                                                                                                                         Length 3921;
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                                                                                                                                                                                TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FROM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,891A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BASTIAN, Kevin L.
NAME: BASTIAN, Kevin L.
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APPLICANT: Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1424 TGTCATTAGGCCTTTCAACTAATAACCTTAGTGGTCCAATACC 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1304 ACTTGAGCGGTTCGATCCCGTTGGCCATAGGAAATCTTACTGAACTTAATATCTTACTGC 1363
                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1244 CTCTTCCATCATCGTTGGGCAGGCTTAAAAACTTAGGCATTCTACTCGCCTACGAAAACA 1303
                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 gcttctctggacctataccggacacattaggaaagcttacaaggctaagattcttgcgtc 325
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Embarcac
CITY: San Francisco
STATE: California
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Song, Wen-Yuang
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                                                                                            join(512..3149, 3993..4393)
                                                                                                                                                             DNA (genomic)
       /product= "RRK-B"
/product= "RRK-B"
/note= "xa21 Xanthomonas spp. disease
/note= "xa21 Xanthomonas rice (Oryza
  resistance gene RRK-B sativa)"
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Query Match

3.2%;

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Length 5992

Query Match Best Local Similarity Matches 122; Conserv

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Mismatches

3.2%;

Score 57.2; DB 6; Pred. No. 4.1e-06;

Length 4517; Indels

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; TOPOLOGY: 11; MOLECULE TYPE: PCT-US93-06251-83
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                                                                                                                                    TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ALGORITHM S. 101619110, Frank S. 101619110, Frank S. 101619110, IUMBER: 31,346

REFERENCE/DOCKET NUMBER: 856

TELECOMMUNICATION INFORMATION: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
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TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
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                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 11530
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                                                                    STRANDEDNESS:
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                       DNA (genomic)
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Mismatches 169; Indels
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; LOCATION:
US-08-238-163-3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-903
INFORMATION FOR SEQ ID NO: 3:
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1558 ATAAAGTCTGATGTCTGGTCATTTGGAATTCTGCAAACAGAACTAGTAAC 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                     190 aataacataagtggaccaattcctagtgatcttgggaatctgacaaatttggtgagcttg 249
                                                           Local 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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ACTAATCTCACCGGAACAATTCCACCTGCAATTGCGAAGCTCACAAATCTCAAAATGTTA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: Townsend and Townsend Khourie and Crew
T: Steuart Street Tower, One Market Plaza
San Francisco
: California
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                                                                       h 3.0%;
Similarity 51.7%;
25; Conservative
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STOTZ, Henrik
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                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                     DNA (genomic)
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                                                                     Score 54.8; DI
Pred. No. 1.2e
0; Mismatches
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                                                                     DB 1;
1.2e-05;
nes 117;
                                                                                                         Length 2075;
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US-08-475-891A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ronald
APPLICANT: Wang,
APPLICANT: Song,
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/373
FILING DATE: 17-CAN-1995
ATTORNEY_AGENT INFOCMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE_POCKET NUMBER: 0237
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                      LENGTH: 6.556 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
KOLECTY' -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,89:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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  NAME/KEY: CDS
LOCATION: JOIN (164E
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                FEATURE:
                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
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Two Embarcadero Center, Eighth Floor
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Song, Wen-Yuang
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join(1648..4383, 5178..5513)
WARTION: /product= "RRK-F"
WARTION: /note= "Xa21 Kanthomonas spp. disease
WARTION: resistance gene RRK-F from rice (Oryza
WARTION: sativa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1995
                                                                                                                                                  DNA (genomic)
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Query Match

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Score 53.8;

DB 3;

Length 6256;

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                                                                                                                 NAME: Bastlan, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
TELEPHONE SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
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                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION UNMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION UNMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION OBTA:
APPLICATION UNMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BASTIAID, KEVID L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3065 ACACACTCTCAAACCTCACAA 3085
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                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 agctttacagcaataacataagtggaccaattcctagtgatcttggggaatctgacaaatt 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 tgtcactgactaatattacaa 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                          TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTTACTGAACTTAATATCTTACTGCTCGGCACCAACAAATTCAGTGGTTGGATACCAT 3064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Application US/08567375 5952485
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                                                        linear
                                      DNA (genomic)
                                                                            single
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                                                                                                                                                                                                                                                      023070-058930
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0; Mismatches 92; Indels
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; LOCATION: join(1648..4383, 5178..5513);
; OTHER INFORMATION: /product= "RRK-F"
; OTHER INFORMATION: /note= "Xa21 Xantho);
OTHER INFORMATION: resistance gene RRK;
; OTHER INFORMATION: (Oryza sativa)"
US-08-567-375-1
Search completed: June 23, 2000, 22:42:10 Job time: 40076\ \text{sec}
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Best Local Similarity 54.2%;
Matches 109; Conservative
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                                                                                                         3065 ACACACTCTCAAACCTCACAA 3085
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                                                                                                                                            tgtcactgactaatattacaa 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "RRK.F"
/note= "Xa21 Xanthomonas spp. disease
resistance gene RRK-F from rice
(Oryza sativa)"
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Pred. No. 4.2e-05;
0; Mismatches 92;
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Perfect score:
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           US-09-180-798-2
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Gapop 10.0 , Gapext 1.0
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em_est2: *
em_est4: *
em_est4: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

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JOURNAL
MEDLINE
COMMENT
                                                                                             REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
AA738547
LOCUS
DEFINITION
                                                                                                                                                                                                                                  SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                         AA738547 656 bp mRNA
SDRLK5 Sorghum bicolor cv. TX430 leaf Sorghum
SDRLK5 similar to protein kinase, highest sim
receptor-like protein kinases, mRNA sequence.
AA738547
AA738547.1 GI:3421472
1 (bases 1 to 656)
Annen, F., Chang, J.-L., Paterson, A.H. and S Characterization of 14 different putative clones of the C4 plant Sorghum bicolor Mol. Gen. Genet. 259 (1), 115-122 (1998) 98409267
On Nov 29, 1993 this sequence version repl
                                                                                                                                                                                   sorghum.
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Lillopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match Length
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TX430 leaf Sorghum bicolor cDNA cli
kinase, highest similarity to
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  replaced
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AW224241 EST300968
C22490 C22490 Rice
AI937984 sc06e07.y
AWZ01125 se98b06.y
AQ271213 nbxb0025I
AI729170 BNLGH1128
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AA738544 SDRLK2 SO
AA738544 SDRLK2 SO
AW233982 Sf33905. y
AA738545 SDRLK3 SO
AA738545 SDRLK3 SO
AA738545 SDRLK3 SO
AA738546 SDRLK4 SO
AA73854 SDRLGH133
AA738546 SDRLGH133
AA738546 SDRLGH132e
D25047 RICR2976A R
AA73856 N201132e
D25047 RICR2976A R
AA73856 TEST244646
B09168 T2E10-T7 TA
AA7367316 LERUM53TR
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                                                  ggttcgccaatggagcggcctaagatgtcagaggtagtccgaatgcttgaaggtga 1613
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                          GGCTCCCCGTTGGACCTCCCAAAGATGTCGGAGGTGGTGAGGATGCTCGAAGGTGA
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Institut fuer Entwicklungsbiologie und Molekularbiologie
Pflanzen.
Heinrich-Heine-Universitaet
Universitaetsstrasse 1, 40225 Duesseldorf, Germany
Tel: (49)-211-81-14871
Fax: (49)-211-81-14871
Email: stockha@uni-duesseldorf.de
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/db_xref="taxon:4558"
/clone="SpRIK5" |
/clone=lib="Sorghum bicolor cv. TX430 leaf"
/dev_stage="green"
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/note="Organ: leaf; Vector: Lambda ZAP II; Site_1: 1
Site_2: Xho I; leaf cDNA library from green leaves,
unidirectionally cloned"
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/strain="cv. TX430"
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                                                               gtttctgcatgacaccaacagagcggcttcttgtatatccatacatggctaatggaagtg
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                                             GTTTCTGTACAACAAAAAAGAGCGCCTGCTTGTTTATCCTTTCATGCACAATCTTAGTG
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SbRLK2 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cr
SbRLK2 similar to protein kinase, highest similarity to
receptor-like protein kinases, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Institut fuer Entwicklungsbiologie und Molekularbiologie
Pflanzen
Heinrich-Heine-Universitaet
Universitaetsstrasse 1, 40225 Duesseldorf, Germany
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Site_2: Xho I; leaf cDNA library from green leaves,
unidirectionally cloned"
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/db_xref="taxon:4558"
/clone="SbxLK2"
/clone_lib="Sorghum bicolor cv. TX430 leaf"
/dev_stage="green"
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                                                                                                                               Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW233982 532 bp mRNA EST 13-DEC-1999 sf32905.y1 Gm-c1028 G1ycine max cDNA clone GENOME SYSTEMS CLONE Gm-c1028-1713 5' similar to TR:023921 023921 SOMATIC EMBRYOGENES RECEPTOR-LIKE KINASE.; mRNA sequence.
                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
Unpublished (1999)
On Feb 18, 1999 this sequence version rep
Contact: Shoemaker R/Public Soybean EST F
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                 Glycine max
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             tatttgcatgaccattgtgatcccaagattatccatcgtgatgtaaaagctgcaaatata 1182
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                                                                                                             CCGCCACTTGGCCTGGCCAGAACGGAAGCGTATTGCATTGGGATCTGCAAGGGGGGCTTGCT 181
                                                                                                                                                                    TATCCTTACATGGCTAACGGAAGTGTAGCATCATGTTTACGAGAACGTCAAGAATCCCAA 121
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                                                     TATTTGCATGATCATTGTGACCCTAAGATTATTCACCGTGATGTCAAAGCAGCTAATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 403.
Location/Qualifiers
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/clone_lib="Gm-c1028"
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/lab_host="DH10B"
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/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                19.9%;
                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                   Score 361; DB 79;
Pred. No. 3.6e-75;
0; Mismatches 106;
                                                                                                                                                                                                                                                                                                            Length 532;
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                                                                                      1265 ctgctgtaaggggtaccttgggctacatagctcccgagtacctctcgactggaaagtcat 1324
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CAGAGAAAACTGATGTTTTTGGGTATGGTATCATGCTTTTTGGAGCTTATAACTGGACAGC
                                                                    CTGCTGTACGTGGCACAATTGGACATATTGCTCCTGAGTATCTCTCTACTGGAAAATCTT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 555)
Blewitt,M., Matz.E.C., Davy,D.F. and Burr,B.
ESTs from developing cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI728030 555 bp mRNA EST 11-JUN-1999 BNLGH19629 Six-day Cotton fiber Gossypium hirautum cDNA 5' simito (U93048) somatic embryogenesis receptor-like kinase [Daucus carota], mRNA sequence.
AI728030 AI728030.1 GI:5046816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 516-344-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: T3 Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: burr@bnlux1.bnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Ben Burr
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                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="Immature fiber"
/dev_stage="Six days post anthesis"
/lab_bost="XXI-Blue"
/note="Vector: pBluescript II KS+"
a 100 c 147 g 162 t
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
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77.58;
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                                                                                                                                                                                                                              Score 352.6; DB 51; Length 555; Pred. No. 3.5e-73;
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1 (bases 1 to 1435)

1 (bases 1 to 1435)

Annen, F., Chang, J.-L., Paterson, A.H. and Stockhaus, J.

Characterization of 14 different putative protein kinase clones of the C4 plant Sorghum bicolor

Mol. Gen. Genet. 259 (1), 115-122 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Gen. Genet. 259 (1), 115-122 (1998)
98409267
On Nov 29, 1993 this sequence version replaced g1:636085.
Contact: Stockhaus J
Institut fuer Entwicklungsbiologie und Molekularbiologie of Pflanzen
Pflanzen
Heinrich-Heine-Universitaet
Universitaetsstrasse 1, 40225 Duesseldorf, Germany
Tel: (49)-211-81-14951
Fax: (49)-211-81-14871
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SbRLK3 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cI
SbRLK3 similar to protein kinase, highest similarity to
receptor-like protein kinases, mRNA sequence.
AA738545
AA738545.1 GI:3421470
EST.
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/dev_stage="green"
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/note="Organ: leaf; Vector: Lambda ZAP II; Site_1:
/note="Organ: leaf; Vector: Lambda ZAP II; Site_1:
/note="Organ: leaf; Vector: Lambda ZAP II; Site_1:
// display in the content of the content
                                                                                                                                                                                      /organism="Sorghum bicolor"
/strain="cv. TX430"
/db_xref="taxon:4558"
/clone="Sbrik3"
/clone=lib="Sorghum bicolor
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DEFINITION

A1900110 538 bp mRNA EST 06-DEC-1999 sc01a04.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLO Gm-c1012-871 5' similar to TR:023921 023921 SOMATIC EMBRYOGEN

CLONE

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REFERENCE
AUTHORS
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                                                                                     TTACAAGGACACGCATGTGACAACTGCTGTACGGGGCACTATCGGGGCATATAGCTCCTGA 60
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On Jun 5, 1998 this sequence version replaced g
On Jun 5, 1998 this sequence version replaced g
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR-LIKE KINASE. ;, mRNA sequence. AI900110 AI900110.1 GI:5606012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
cail: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Seq primer: -40Rp from Glbco
High quality sequence stop: 411.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean, EST Project
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Shoemaker, R., Keim,
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                                                                                                                                                                                                                                                                                                                                                                                                            /note-"vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from the apical shoots of 9 to 10 day old etiolated seedlings. The shoot tips including any emerged leaves were harvested for mRNA isolation. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XIIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                                                     Erpelding."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Glycine max"
/db_xref"*taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1012-871"
/clone_11b="Gm-c1012"
/tlssue_type="Apical shoot tips, 9-10 day old etiolated
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Shoemaker R/Public Soybean EST Project
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Pred. No. 2.6e-68;
0; Mismatches 115
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U.
                                                                                                                                                                                                                                                                         Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                          Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3137451
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                                                                                                                                                                                                                                                          dfrisch@CLEMSON.EDU
/tissue_type="callus"
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/dev_stage="25-40 days old"
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                                                                                                                    /db_xref="taxon:4081"
/clone="cLEC14J5"
                                                                                                 /clone_lib="tomato callus,
                                                                                                                                                                                                                     ocation/Qualifiers
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      EST.

upland cotton.

upland cotton.

Gossypium hirsutum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core

eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 597)

Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.

ESTs from developing cotton fiber

Unpublished (1999)

On Jun 5, 1998 this sequence version replaced gi:3187180.

Contact: Ben Burr
                                                                                                                                                                                                     carota], mRNA sequence.
AI727837
AI727837.1 GI:5046689
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BNLGE19209 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to (93048) somatic embryogenesis receptor-like kinase [Daucus
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Pred. No. 5.6e-56;
0; Mismatches 172;
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                                                                                                                                                                                                                                           gtacccagggttcgccaatggagcggcctaagatgtcagaggtagtccgaatgcttgaag 1609
                                                                                                                                                                                                                                                                                                               acctggagaacaattacattgacacagaagttgagcagcttattcaagtagcattactct 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcattactggacagagagcttttgatcttgctcgccttgcgaacgatgatgatgttatgt 1429
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                                                                                                                                                       NANANGGGCNCNCNNANANGTGGGANGAATGGGCGCCCGTTGAGGTCCT
                                                                                                                                                                                                                                                                                                                                                                TTCTTGACTATGTCAAGAAGCTGGAAAGGGAAAAAAACCTGGATGCTATCGTAGATCATA
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                                                                                                                                                                                                                                                                                           ATCTTAATAAAATTACAACATGGAGGACGTAGAGGCAATGATCCAAGTTGCATTGCTTT
         AA738546 655 bp mRNA EST SDRLK4 Sorghum bicolor cv. TX430 leaf Sorghum bicolor SDRLK4 similar to protein kinase, highest similarity receptor-like protein kinases, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Upton, NY 11973, Tel: 516-344-3396
Fax: 516-344-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
receptor-like
AA738546
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/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/dev_stage="Six days post anthesis"
/lab_host="xil-Bile"
/note="Vector: pBluescript II KS+"
5 a 107 c 165 g 148 t 12 ot
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Pred. No. 9.5e
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MEDLINE
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Best Local Similarity 65.3%;
Matches 412; Conservative
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                                                                        actaggatctgctagggggctttcttatttgcatgaccattgtgatcccaagattatcca 1157
                                                                                                                                         tttaagagagcgtcagccatcagaacctccccttgattggccaactaggaagaggattgc 1097
                                                                                                                                                                                                          gacaccaacagagcggcttcttgtatatccatacatggctaatggaagtgttgcgtcgtg
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                                                   TATAGGCACAGCTCGTGGACTGGAGTATATGCACGAGCACTGCAATCCTAAGATTATACA
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Annen, F., Chang, J.-L., Paterson, A.H. and Stockhaus, J.
Characterization of 14 different putative protein kinase clones of the C4 plant Sorghum bicolor
Mol. Gen. Genet. 259 (1), 115-122 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98409267
On Jan 13, 1998 this sequence version replaced gi:3421471.
Contact: Stockhaus J
Institut fuer Entwicklungsbiologie und Molekularbiologie d
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Universitaetsstrasse 1, 40225 Duesseldorf,
Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
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Poaceae; Sorghum
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/dev_stage="green"
/note="Organ: leaf; Vector: Lambda ZAP II; Site_1:
Site_2: Xho I; leaf cNNA library from green leaves,
unidirectionally cloned"
a 124 c 179 g 183 t
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/clone-"SbRLK4"
/clone_lib-"Sorghum bicolor cv. TX430 leaf"
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Pred. No. 3.1e-53;
0; Mismatches 213;
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                                                                   atacccatgttacaactgctgtaaggggtaccttgggctacatagctcccgagtacctct 1309
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                                           ATGAAGATTTTGAAGCAGTTGTCGGTGACTTTGGCCTTGCGAAGTTGGTGGATGTGAGGC
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Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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1 (bases 1 to 703)
Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
ESTs from developing cotton fiber
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Brookhaven National Laboratory
Upton, NY 11973, USA
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On Jun 5, 1998 thi
Contact: Ben Burr
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Fax: 516-344-3407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: burr@bnlux1.bnl.gov
                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             /Organism="Gossypium hirsutum"
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/Gultivar="Acala Maxxa"
/Glone_lib="%15x-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="%51x days post anthesis"
/note="Vector: pBluescript II KS+"
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Pred. No. 5e-4:
0; Mismatches
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5e-49;
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
On May 7, 1998 this sequence version I
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, Ut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J. Martin, G.B., Tanksley, S.D. and Glovannoni, J. Generation of ESTs from tomato carpel tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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EST244774 tomato ovary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 864 656 4366 Fax: 864 656 4293
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     136
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     respectively
88 c
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SOURCE
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Best Local Similarity 67.8
Matches 312; Conservative
                                                                                                                                                                                                                                          JOURNAL
MEDLINE
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A087p60u Hyb
tremuloides
                                                                                                                                                                                                                                                                                                      1 (bases 1 to 380)
Sterky, F., Regan, S., Karlsson, J., Hertzberg, M., Rohde, A.,
Holmberg, A., Amini, B., Bhalerao, R., Larsson, M., Villarroel, R.,
Montagu, M., Sandberg, G., Olsson, O., Teeri, T.T., Boerjan, W.,
Gustafsson, P., Uhlen, M., Sundberg, B. and Lundeberg, J.
Gene discovery in the wood-forming tissues of poplar: Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                          Populus tremula x Populus tremuloides.
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eubylicphytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                   Royal Institute of Technology (KTH)
Teknikringen 34, S-100 44 STOCKHOLM,
Tel: +46 8 790 8287
Fax: +46 8 24 54 52
                                                                                                                                                                                                                                                            5,692 expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI165643.1
FORWARD: AAAGGGGGATGTGCTAGGCGBACKWARD: GCTTCCGGCTCGTATGTTGTGTG
                                                                                                                                                                           Department of Biotechnology
                                                                                                                                                                                              Contact: Sterky F
                                                                                                                                                                                                                     On Jan 17, 1998 this sequence
                                                                Email: fredrik@biochem.kth.se
                                              PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 bp mRNA EST 03-DEC-1998 Hybrid aspen plasmid library Populus tremula x Populus des cDNA 5', mRNA sequence.
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Pred. No. 1.3e-42;
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                                                                                                                                    Sweden
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of.

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RESULT 13
AW310334/c
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VERSION
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                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                    DEFINITION
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Best Local Similarity
                                                                                                                                                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgccttgcgaacgatgatgttatgttgttggattgggttaaaagccttttgaaagag 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGCTGNCAAAATTGATGNACTACAAGGATACGCATGTCACCACTGCTGT-CGTGGTACA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAGCTAGAAATGCTAGTCGATCCTGATCT-CAAAACAAATATGTGGAAGCTGAGGTG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCTGGCAAATGATGACGATGTCATGTTACTTGATTTGGGTAAAAGGACTTCTCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGGGTATGGAATCATGCTTCTGGAGCTAATTACTGGACAGAGGGCTTTCGACCTTGCC 239
                                                                                                                                                                                                                                                      AW310334 412 bp mRNA EST 21-JAN-2000 sf34f03.x1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-1878 3' similar to TR:023921 023921 SOMATIC EMBRYOGENESIS RECEPPOR-LIKE KINASE. ;, mRNA sequence.
                                                                                              Glycine max

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnollophyta; endicotyledons; core

eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
1 (bases 1 to 412)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Shomma,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Marti
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., A
                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: CGTTGTAAAACGACGCCAG High quality sequence stop: 380.
                                                                                                                                                                                                                       AW310334
AW310334.1 GI:6725935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Onote-"Vector: pBluescript SK; Site_1: SalI; Site_2: NotI Cambial region tissues, including developing xylem, the meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. CDNA was prepared and cloned into lambda gt22a. DNA was isolated and subcloned into pBluescript SK using SalI and NotI restriction enzymes."

a 67 c 99 g 102 t 3 others
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/db_xref="taxon:47664"
/clone_lib="Hybrid aspen plasmid library"
/tissue_type="Cambial region"
/dev_stage="1.5 m actively growing tree"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.2%;
76.7%;
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Pred. No. 5.3e-42;
0; M1smatches 87;
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Theising, B., Allen,
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1300 gagtacctctcgactggaaagtcatcagagaagaccgatgtctttggttatgggattatg 1359

GAGTTTCTCACAACTGAAAGGTCTTCAGAGAAGACTGATGTTTTTGGCATATGGCATCATG

412 GATCACACACATACTCATGTTACTACTGTTGTATNCCGTACGCATGGCCAAATAGCACAC

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1240 gattacaaggatacccatgttacaactgctgtaaggggtaccttgggctacatagctccc 1299
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Washington University School of Medicine
Washington University School of Medicine
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McCann,R., Waterston,R. and Wilson,R.

McCann,R., Waterston,R. and Wilson,R.
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On May 18, 1998 this sequence version replaced gi:3138263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trace considered overall poor quality High quality sequence stop: 1.
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                                                                                                                                                                                                                                                                             107
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314 286 1810
                                                                                                                                                                                                                                                           first-strand synthesis primer was used. An 'anchor' nuclectide (V=A,C, or 6) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGTAGTCGAGG(T)]8V] to anchor the primer [GAGAGAGAGAGAGAGAGTACTGAGTCGAGG(T)]8V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcobRL Life Technologies' cDNA size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested with EcoRI and XhoI, and phosporylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium japonicus, strain USDA110 priot to harvest. Stratagene's CDNA synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's
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/lab_host="DH10B"
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/clone_lib="Gm-c1028"
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/db_xref="taxon:3847"
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Khanna,A., Bolla,B., Marra,M., Hilller,L., Kucaba,T., Martin,J.,
Rhanna,A., Bolla,B., Consoud,K., Steptoe,M., Theising,B., Allen,M.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
MCCann,R. Watterter, P. and Waller, J., Jackson,Y., Cardenas,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI416897 474 bp mRNA EST sal9e11.x1 Gm-c1005 Glycine max cDNA clone (Gm-c1005-165 3' similar to TR:023921 023921
                                                                                                                                                                                                                               This clone is available through: Genome Systems, Inc. 4 Parkway Circle St. Louis, Missouri 63134 For further it call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-33 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com Possible reversed clone: similarity on wrong strand Seq primer: T7 E7 from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, I Tel: 314 286 1810
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/note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhOI; This library was constructed by Dr. Randy C. Shoemaker and Dr. John Erpelding, USDA-ARS Agronomy Department, G401 Agronomy Hall, Iowa State University,
                                                                                                                  /clone="GENOME SYSTEMS CLONE
/clone_lib="Gm-c1005"
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/db_xref="taxon:3847"
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                                                                                                                                        Generation of ESTs from tomato callus Unpublished (1999) on May 18, 1998 this sequence version Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum Eukaryota; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                      Tel: 864 656 4366
Fax: 864 656 4293
                                                                   Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                        Alcala, C., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
                                                                                                                    Clemson University Genomics
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    dfrisch@CLEMSON.EDU
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Search completed: June 23, 2000, 19:06:03 Job time: 27396 sec
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Best Local Similarity 66.3%;
Matches 299; Conservative
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/tissue_type="callus"
/tissue_type="callus"
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/cultivar="TA496"
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-318.517 Million cell updates/sec
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57: gb_htg11:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C CCC 335	000 00 22222222222222222222222222222222	c 1186 c 119 222223235	00 00 00 00 00 00 00 00 00 00 00 00 00	Result NO. 1 2 2 3 C 4
99.2 99.2 97.4 97.2 97.2 96.3 96.3 93.6	1346667710	2011122285	387.4 375.6 289.6 277.2 273.2 270.8 270.8 270.8 270.8	
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ALIGNMENTS

Db 301 ACADACTCAAATCTTTCAACTCTCTCCCAAAGTTGGGTTTAGAAGAATATCAGC 360 Qy 361 BBBCGCtBBLATCTLTTCTGCATGTTTCATCGCATAGTTGGGTTTAGAAGAAGATTATCAGC 360 Qy 361 BBBCGCTBBLATCTTTATTGTTGCATGGTTTATCAAAATTCACAAAATTCACAACCATTGTAA 420 Db 361 ACADACACTAATATCTTTATTGTTGCATGGTTTATCAAAAATTCACAAAATTCACAACCATTGTAA 420 Qy 421 BBBBBBLATCACATTTTTGGTATGAGATTGCCCACATGATAGTGAAACCTCTTTAACATTT 480 Qy 421 AAAAAAATTCACATTTTTGGTATGAGATTGCTCACATGATAGTGAAACCTCTTTAACATTT 480	181 TGGTATTGTGAAACAGTAGTAAAGTCATATCGGGCACGCCATACTACTTCCACAGTG 241 gaacttggccaaattttgtctttgccgtctctacagtttcttcacccaaattttttgttg [1][][][][][][][][][][][][][][][][][][]	61 aatgtgtgatatttaaagggtaacaaatgtaatctgctttttattttactttttacctct 1	Query Match 100.0%; Score 4081; DB 5; Length 4081; Best Local Similarity 100.0%; Pred. No. 0; Matches 4081; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 4081; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 tctagaaaccttttgatcataatgaaaataaagagtccatcaaccacatggggtaagcat 60	exon 12801367 exon 17961928 exon 20142085 exon 22032346 exon 24502521 exon 26172688 exon 26172688 exon 30153446 exon 37604081 BASE COUNT 1120 a 770 c 785 g 1406 t	REFERENCE 1 (bases 1 to 4081) AUTHORS De.V.S., Schmidt,E.D., Van,H.G. and Hecht,V.F. TITLE PRODUCTION OF APOMICTIC SEED JOURNAL PAtent: WO 9743427-A 20-NOV-1997; CIBA GEIGY AG (CH) FEATURES Location/Qualifiers 1.4081 90urce 1.4081 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /clone="RAABIDOPSIS SERK GENE"	RESULT 1 A67815 A67815 A67815 LOCUS A67815 A67815 A67815 DEFINITION Sequence 20 from Patent W09743427. ACCESSION A67815 VERSION KEYWORDS CHAIC cress COURCE CHAIC cress COURCE CHAIC cress COURANISM Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Embryophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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1380	ttacttccgaatcattcactgtggcttgcttctgctaatttggaaggttcgtggttac	N	Qy
1320	TTTAGCATTGTTTGAAATGGAGTCGAGTTATGTGGTGTTTATCTTACTTTCACTGAT	1261	ДĎ
1320	tragcattgttgttgaaatggagtcgagttatgtggtgtttatcttactttcactga		Qγ
1260	TGGTGATTTTCGGAAGTTAGGGTTTTCTCGGATCTGAAGAGATCAAATCAAGATTCGAAA	1201	đđ
1260	ggtgattttcggaagttagggttttctcggatctgaagagatcaaatcaagattcgaa	1201	Qy
1200	AAGGGTTATCGAAAAAATGAGTGAGTTTGTGTTGAGGTTGTCTCTGTAAAGTGTTAATGG	1141	Дb
1200	ggttatcgaaaaaatgagtgagtttgtgttgaggttgtctctgtaaagtgttaatg	1141	Qy
1140	ATTAGGATTTTATTTTTTTTACTCTTTGTTTTAATGCTAATGGGTTTTTAA	1081	Дb
1140	ttaggatttttattttatttttactctttgtttgttttaatgctaatgggttttta	1081	Qy
1080	GTGTGTGAGAGAGAGAGTGTGGTTTGATTGAGGAAAGACGACGACGAGAAACGCCGGAG		ДĎ
1080	tgtgtgtgagagagagtgtggtttgattgaggaaagacgacgacgacgacgccgga	1021	Qy
1020	TTTTTG	961	Дb
1020	ctcttattttttttttaaaaaaaaaagtttcatctttattcaactttttgttttacag	6	Qy
960	GTTGCGGCTTAATAAAAAGCTCTTTTGTTATTATTACTTCACGTAGATTTTCCCCCAAAAA	901	дb
960	ttgcggcttaataaaaagctcttttgttattattacttcacgtagattttcccccaaaa	Ö	Qy
900	AGAAGAAAAGAGAGGAACAACAACACACACTAATCATAGTTTCTCTGGCAGGCTTGTT	841	Db
900	gaagaaaaagagaggaacaacaacaacacactaatcatagtttctctgggcaggcttgt	841	Qy
840	CCCGTTGAGATCTTTAAAAATATTAAATATATCAACGAAAAAAGCTATTTTATTCATA	781	Db
840	ccgttgagatctttaaaaatattaaataatatcaacgaaaaagctattttattcat	781	Qy
780	TACGGGCAGCTTATATTCCTCGTCTTCCTCTTACACCACTGCATGCCCCATAAATAA	721	Дb
780	acgggcagcttatattcctcgtcttcctcctctacaccactgcatgcccataaataa		Qy
720	CATCTCTTCTCCCCCGAACCCGTTTTTTTGACCGGTCAGTTCGGGCAGCAGCACCGT	661	Db
720	catctcttctctcccccgaacccgttttttttgaccggtcagttcgggcagcagcaccg	661	Qy
660	TGCATAGCCTTAAGAGCTTTCAACTTTACCCCAAAACCCAAAGCGATGTCACTTTCAA	601	Дb
660	gcatagccttaagagctttcaactactttaccccaaacccaaagcgatgtcactttc		Qy
600	GTTTTTCTACTTAAAGAAAAAAGGGACCCAACAGAGAGAG	541	Db
600	tttttctacttaaagaaaaagggacccaacagagagaggtttgaccaggagaaacg	541	Qy
540	TAACTTTACTTTCATAAATACGGGATTACGAATCTTACTTGCATTAAAAATTTAGAAAAG	481	οь
540	aactttactttcataaatacgggattacgaatcttacttgcattaaaaatttagaaaa	481	Qy

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Submitted (10-DEC-1999) Plant
Street, Albany, CA 94710, USA
On Dec 10, 1999 this sequence
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Liu,S.X., Lee,J.M., Sakano,H., Yu,G., Jhaveri,A., Lenz,C.,
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Toriumi,M., Chin,C., Chiou,J., Choi,E., Gonzalez,A., Howng,B.,
Toriumi,M., Chin,C., Chio,P., Vaysberg,M., Altafi,H., Brooks,
Koo,T., Li,J., Liu,A., Pham,P., Vaysberg,M., Altafi,H., Brooks,
Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N.,
Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Nguyen,M., Palm,C.,
Shinn,P., Tambunga,G., Davis,R.W., Ecker,J.R., Federspiel,N.A.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
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2159	2100 tycatcatyctttaacaaaacaaatccaagatttyacagaagaagcactygagttacctt	VQ.
2099 78655	2040 gccatttagttccagagcttggtgtgctcaagaatttgcagtatttgtaagttccactta 	p 8
2039 78595	1980 ttaccgacatttttgtttcttttgtcaaatacagtgatttggggaatgcagagttatctg 	ду 2 9
1979 78535	1920 cataagagtgtaaagctttcttctactaatcccactttttaaactttgacctcagcgtgg 	B 8
1919 78475	1860 toctacgctagtgaatccttgcacatggttccatgtcacttgcaacaacgagaacagtgt	B 성
1859 78415	1800 tgctttgcatactttgagggttactctagttgatccaaacaatgtcttgcagagctggga 	D 64
1799 78355	1740 aattagacttttcaccaattgatgctaattgtgtagatttgttgttcttgttataggtga 	gg dg
1739 78295	1680 aatttgtttaattattagcctctaatctcagagaggcctgtttgaatagttctctcttga 	B 8
1679 78235	1620 attgatgttgatccaaacattctctgaaagacttcatttgtttttggttttgtaaag 	Db Qy
1619 78175	1560 tttgtatattgtaaaggcatgttctttgggttgaaaagctgggttatttgatatcttaag 	рь Оў
1559 78115	1500 tytaagatttagtggctagtactttgaatacactgttttgctttttcttgttcagatcaac	g 49
1499 78055	1440 gaatogctatotttagtgtotgoattttgatttatgaaaattgttgttgttgttotttgtatt 	B 성
1439 77995	1380 tcaattactcagctttactcgtttctcaattactttctcgattcttttttatttggaggt	g 8
1379 77935	1320 tottacttoogaatoattoactgtggcttgcttctgctaatttggaaggttcgtggttac 	g 8
1319 77875	1260 atttagcattgttgtattgaaatggagtcgagttatgtgggtgtttatcttactttcactga 	р 9
1259 77815	1200 gtggtgattttcggaagttagggttttctcggatctgaagagatcaaatcaagattcgaa 	DP QA
1199 77755	1140 aaagggttatcgaaaaaatgagtgagtttgtgttgaggttgttctctgtaaagtgttaatg 	р 9
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1 (bases 1 to 88401)

Vysotskaia,V.S., Schwartz,J.R., Yu,G., Toriumi,M., Lenz,C., Liu,S., Lee,J., Liu,A., Li,J., Kremenetskaia,I., Luros,J., Gonzalez,A., Lee,J., Liu,A., Li,J., Kremenetskaia,I., Luros,J., Gonzalez,A., Altafi,H., Araujo,R., Chao,Q., Conn,L., Conway,A.B., Dunn,P., Hansen,N., Hulzar,L., Kim,C., Palm,C., Rowley,D., Shinn,P., Walker,M., Davis,R.W., Ecker,J.R., Federspiel,N.A. and Theologis,A. Arabidopsis thaliana chromosome 1 BAC F23M19 sequence Unpublished (1999)
                                                                                                                                                                                                                                                                                         Submitted (17-JUN-1999) Plant Gene Expression Center, 800 St., Albany, CA 94710, USA On Jun 17, 1999 this sequence version replaced gi:4996902. The sequence of BAC F23M19 from Arabidopsis thaliana chrom Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        submitted (04-JUN-1999) Plant
Street, Albany, CA 94710, USA
4 (bases 1 to 88401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-MAY-1999) Plant street. Albany, CA 94710, USA
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3 (bases 1 to 88401)
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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complement(j0in(796. .1116,1205. .1271,1349. .1432,
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domain."
                                                                                                                                                                                  /clone="F23M19"
codon_start=1
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thaliana
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                                    PF(00561 alpha/beta hydrolase fold
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GVAHCSLFQDRLKDFKNDSKLKAKLQNTCRGPNDPSVVLDQMTPLEVDNQIYKOIKSQ
RGILRIDQNLGLDDSTSRIVSNFALNETLFGERFAEANQINGEIKVLTGNSGEIRTNC
IVVSH"
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EFHFIGDAILRYFRCRVNLIZWADSPLYHGVVSRCQILHGRYVATFWILASPHIOTCFL
NFHGLEPVFTYTRQLFLTXSDGGTIALDWLTNSDVLDGSLHNKSEITKEDTTFIAVUT
GLTSDSSSAYLKHLAKDTAKTGWNVISNHRGLGGVSYTSDCFYNAGWTDDIRVLDY
LQHKYPRAPLFAIGTSIGANVLVKYLGEEGEKTPLRGAVAICSPWDLLIGDRFICRTL
KQKLYDKALTTGLQGYAQLHEPQFTLKLANWEGIKKSRSIRDFPNHATCLVGKETTVDT
YYRKSSTQYVGNVAVFLLCISALDDPLCTKEAIPWDECRANKNIVLATTNHGGHLAF
FEGLTGSSLWWYRATNEFLGVLSGSFYMHIGKTVDKRSGSGKGEFSINGGFYLNGGFLAF
DGLVAAVKYEQDTNKTTLKQRGRKPEEDVTKKSFKELCRQTKQSVWWLGYIGMVTSFP
LLGMLLNYIFRKKGRFTTTSG"
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EVANTIVKGANLMHSLSKDSITHLKEVVLPSEGEVQNLIKSGMDELLRIAAADKRFQHD
EVANTIVTGRDLXHELHALDRFEQDYQLKIQEEEMPSTAQRGVCDTLAILRTELKSQKK
HVRNLKKKSLMSRILEEVMEKLVDVVHFLHLEIHEAFGGADPDKPANDPPINHKKLGS
AGLALHYANIITQIDTLYSRSSTMPASTRDALYQGLPPSIKSALRSRIQSFQVEEELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23307. .26279. .2355. .23431. .23627,23656. .23751,23850. .2. join(23307. .23355,23431. .23627,23656. .23751,23850. .2. 24002. .24145,24225. .24309,24401. .24491,24571. .24735,24402. .24955,25045. .25117,25210. .25348,25453. .25865,25953. .26140,26231. .26279)
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kvyyepqghielvssislsledefsfeihlfsisllsisvetsfreeimelqpicdlps
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Arabidopsis thaliana."
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HADKEKTEAYILDLVVWLHHLVTQVRATTGYGLRSPVKSPIRSPNQKTIQLSSGSHNP
SMGLPLLTTEDQEMLRDVSKRRKTPGISKSQEFETVAKARLCKHHRLSKSSSHSPMMG
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MSYPVQPMPKLNYNNQMVTEMEEN ITTKTGTNFRLFGVTLDTPPV IKDP IEEIGSEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMMKNKKDTFSTRRPSSVPIIDFDIDRMKALDVIDRVDTIRSL"
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Length

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PNSTEYSTYBSPSPNSFLAAVSFAGSVPIWSAGTVDSRGSLRLHTSGSLRTINGSGT
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FGICSYNDTNPICSCPSRNFDFVDVNDRKKGCKKKVELSDCSGNTMLDLVHTRLFTY
EDDPNSESFFAGSSPCRANCLSSVLCLASVSMSDGSGNCWGKHPGSFFTGYQWPSVPS
TSYVKYCGPVVANTLERATKGDDNNSKYHLMIVAVAVALGLGLVAVEIGLWWCCCRK
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RNFDVSEKTNHKKFSIWAY EEFEKGNTKAILDTRLSEDQTVDMEQVMRWNTISFWGIQ
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COMplement(36027. 36827)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Contains similarity from Zea mays, is a member glycoprotein family and con protein kinase domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLTEGKKFGLSQTLRSPTEIQNKQFSSSRTCTKVQMQGVTIGRAVDLSVLNGYDQLIL
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COMPLEMENT (18888. .31377)
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47284. .47637,47725. .47869,48023. .48613,48703. .48736,
48815. .48860))
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complement(join(43028..4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
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                                                                                                                  cerevisiae
                                                                                                                                                         similarity to
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ber of the PF|00954 S-locus
contains a PF|00069 Eukaryotic
                                                                                                          ty to gi|836774 FAB1 protein genome gb|D50617."
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                                                    TTGCTTGTTTATCCTTACATGGCTAATGGAAGTGTCGCTTCCTGTTTGAGAGGTAACCTT
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                                                                                                                                                                                                                                                       Submitted (11 MAR-1999) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 can by the wed at: http://websvr.mips.biochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 96475)
Bevan, M., Rose, M., Hempel, S., Entian, K.-D., Hoheisel, J.,
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Unpublished
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                                                                                                                                     /organism="Arabidopsis t
/variety="Columbia"
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/chromosome="4"
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complement(join(2377. .2571,2755 .2837,3032. .3098, 3180. .3230,3461. .3574,3668. .3724,3815. .3928))
/note-"similarity to Caenorhabditis elegans cosmid, gene T16G1.11, pID:e1349366; contains EST gb:T20620, N65143, T45799, H36819, R65238, N37318"
                                                                                                  /gene="F17M5.10"
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/note="strong similarity to WD-repeat protein carota, PD:92253631; Contains Trp-Asp (WD-40) signature [VLAIALDHTVYLWDA] [TGGGGGDRTIKFWNT] [VASAAGDETLRFWNV]"
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slivlshyleigrfqqfwdeaaknrhileavpgfeqaiqayashllslsyqkvprsvl
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SRVLYMAQSPDGCTVASAAGDETLRFWNVFGVPETAKKAAPKAVAEPFSHVNRIR"
complement(4688. .4780)
                                                                                                                                                                                                                                                                                                                                                 /translation="MDAGLNRCPLQEHFLPRKNSKENLDRFIPNRSAMNEDYAHFALT EERKGZKOGSANTSSPSKEAYRKOLAFFMNLNHTRILAFENRFOARVELLPSNHSASIH QOPKSVKPRRYIPQTSERTIDAPDIVDFYLNLLDWGSANVLAIALDHTVLYDHOSRYG STSELVTIDESKGPYTSINWAPDGRHYAVGLNNSEVQLWDSASNRQLRTLKGGHQSRV GSLAWNNHILTTGGMDGLIINNDVRIRSPIVETYRGHTQEVCGLKWSGSGQQLASGGN DNVVHIWDRSVASSNSTTQWLHRLEEHTSAVKALAWCPFQANLLATGGGGGDRTIKFW
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5815. .6093,6423. .64
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              /gene="F17M5.50"
12884. 14176
/gene="F17M5.50"
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                                                                     /number=4
12884. .1
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9139. .9417,9803. .99
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LSLAKRA I SPDGFL VFMKRSHVVSKCFLT I PYKWCVKNML I TRQEVVMQVDQTKWEMK
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/number=1
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'note="strong similarity
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YPYELEIWITTKIEAEMVSWNKFLRIDIEPNNNIMVPFIYGGFFIDEEKKKVALGFDE
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HIGKVTSTREGESRVIMLIDYNLFLMSAVLMDDVDPSIEFKGKLSCLKEQVKISQVFH
CEGLLLCILKDDTRIVVMNPYRQETKWIIPRYSHRPYVMNNIRYALGYENNKSGRSLK
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                                     GAAAGCTATGATAATATTTTTTTCTCCTTCATATATTATCACTTTCGCAGTTTTGGCAA
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Daucus carota
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euphyllophytes;
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Sequence 1 from Patent W09743427.
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nilarity 57.8%;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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On Dec 17, 1999 this sequence version replaced gi:4726109.
The sequence and annotation of the sequence and annotation of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6D23, F5J6, T17A5, and T13L16, the ESA group for sequencing clone F13D4, and Scott Jackson, Jining Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes were identified by a combination of three methods: Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thale cress.
                                                                                                                                                                                                                                                                                                                                            This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to the bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis.
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                                                                                                                                                                                                                                                                           all correspondence to:
                                                                                                                                     /organism-"Arabidopsis
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                                                                    /db_xref="taxon:3702"
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                                                                                                                                                                                                                                           ocation
                                                                                                                                                                                                                 .65899
                                                                                                                                                                                                                                           'Qualifiers
                                                                                                                                                                                                                                                                               at@tigr.org.
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   repeat_region
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                                                                                                                                                                                                                                                                complement(18082.
/gene="At2g13700"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<14929. .>17114)
/gene="At2g13690"
/note="F13J11.4; predicted by genscan and genefinder"
complement()oin(14929. .15843,16401. .17114))
/gene="At2g13690"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(<3349. .3541,3644. .3744,4109. .4230,4375. .4471,
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/gene="At2g13670"
/gene="At2g13670"
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LEVLAANSDVFSGLIAEEKKCSSSSSSIGLKNTCRIEVCDVENLGVFRETVELMFEES
MVIIKKFMTMGVYRAIDVLEVAAGIKFSBAVLSGCLKLEAVPPFEDEEEKLRRLEGIY
SFDDDAVSELLARFNSBTENLODSLSKKLVMSITSCSDVMPRNELKSLVKGLLCKSV
VYEKEQPEINKEDIYRAGKCCVDSLAKLFEEGSSSSSSKKEKPLIESISREVENINML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAD28311.1"
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SLASRYKKTDGREVESFYQQYYEHYVRALDQGDQADRAQLGKXQTAGVLFEVLAHAVN
KSEKVERVAPEJIAAARDVDEKENTVAPYNLFLDSSAAGAGSYMQLEFYKAAVAALG
KSEKVERVAPEJIAAARDVDEKENTVAPYNLFLDSSAAGAGDIQQRKILYMGLYLLI
TRGLNMPSGFEQHRKKTGNLDLLDMLRAMFGFQASMLPQAAQDIQQRKILYMGLYLLI
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SPPRNLYLCLRLYLLAFCHRSPEEIEQDEDSNSSYSVPINRINLINPPRRTDALNKPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(517. .842,907. .1114))
/gene="at2g13660"
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/gene="At2g13660"
                                                                                              /rpt_family="POLY_A" complement(29932. .3 /gene="At2g13710"
                                                                                                                                                                                                                                                                                                                                                                                WFSKHGTECPNLSKAFQIWWRRSFLRGVESSTCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(<14929. .15843,16401.
/gene="At2g13690"</pre>
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/gene="At2g13680"
/note="F13J11.3"
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join(3349. .3541,3644. .3744,4199. .4230,4375. .4471,
4583. .4693,4792. .4928,5629. .5755,5848. .5997)
/gene="At2g13670"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETGIKTGNLKHKPKSSD"
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/db_xref="GI:4726112"
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                                                                    mote-"F13J11.6"
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                                                                                                                                                                                                                                                                                                                                              tatgcagccgaagaagatccagaagttcatctgggacagctcaagaggttttcttttgcgg 3357
                                                                                                                                                                               gggaaagtctacaagggacgcttggcagacggaactcttgttgctgtcaagagactgaag
                                                                                                                                                                                                                                                            gagctacaagtggcgagtgatgggtttagtaacaagaacattttgggcagaggtgggttt 3417
GCCGTTCATAGGAACTTGCTTCGGCTTCGTGGCTTTTGCATGACTCCAACTGAAAGATTA
                                                                                                  gaagagcgaactccaggtggagagctccagtttcaaacagaagtagagatgataagtatg
                                                                                                                                                          GGTATATTGTATAAAGGACGTTTAGCTGATGACACTCTAGTGGCTGTGAAACGGCTAAAT
                                                                                                                                                                                                                                       GAACTGCTAGTTGCTACAGAGAAATTTAGCAAAAGAAATGTATTGGGGCAAAGGACGTTTT
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="POLY_A"
complement(<33782...34228)
/gene="At2g13730"
complement(<33782...34228)
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/note="RT3J11.8"
complement(33782...34228)
/gene="At2g13730"
/note="Rt2g13730"
/note="Rt2g13730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(37457. .37522)
/rpt_family="(GAAAA)n"
join(<3893. .39051,39561. .40208)
/gene="At2g13750"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAD28313.1"
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QVMREKNVLSNVDQNKRFFIWDEGSEAALENAFGTSEDKQKKWIEKYVFGTFLDSKKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="(CAA)n"
complement(31832..31913)
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AAEPRRTLGDENRPGMTYANRSAIVPPPYQRNDYESHLFYYITLHI"
complement(35689. .35776)
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/rpt_family="(TAAAA)n"
36924. .37497
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/note-"unknown protein"
/codon_start-1
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/note="F13J11.7"
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/note="F13J11.9"
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.>33473
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                                                                                                                                                                                                                                                                                                                                                                                              Score 375.6; DB 5
Pred. No. 1.5e-61;
0; Mismatches 244
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E 1 (bases 1 to 120787)

Federspiel,N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R.,

Au,M., Araujo,R., Brendel,V., Buehler,E., Dewar,K., Feng,J.,

Kim,C., Li,Y., Oji,O., Osborne,B.I., Shinn,P., Sun,H., Toriumi,M.,

Vysotskaia,V.S., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.

Genomic sequence of Arabidopsis

L Unpublished (1997)

E 2 (bases 1 to 120787)

E 2 (bases 1 to 120787)

E 5 Federspiel,N.A., Davis,R.W., Conway,A.B., Palm,C.J., Conway,A.R.,

Kurtz,D.B., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y., Shinn,P.,

Sun,H., Oji,O., Osborne,B., Shen,Y.K., Toriumi,M., Vyotskaia,V.,

Pirect Submission

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
              Federspiel,N.A., Davis,R.W., Conway,A.B., Palm,C.J.,
Kurtz,D.B., Buehler E., Dewar,K., Feng,J., Kim,C., L.
Sun,H., Oji,O., Osborne,B., Shen,Y.K., Toriumi,M., V.
Yu,G., Theologis,A. and Ecker,J.
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,J., Kim,C., Li,Y., Shinn,P.,
Toriumi,M., Vyotskaia,V.,
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6 (bases 1 to 120787)
Federspiel. W.A., Palm.C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., Uu, G., Ecker, J., Theologis, A. and Davis, R.W.
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Submitted (09-UUL-1997) Biochemistry, Stanford University/DNA
Sequencing and Technology Center, 855 California Avenue, Palo Alto,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAB71954.1"
//db_xref="GI:2462735"
/translation="MCCRWVTLRQNDFGTEVSLSVFGSMDVLVAPIIGFFQKIIVLQI
/translation="MCCRWVTLRQNDFGTEVSLSVFGSMDVLVAPIIGFFQKIIVLQI
LNVTLDLMVRGGTSPQNGYGYVFAVNADKTPCFTASNLERLKSGLEDYVLRHANCLDT
MCDYCFSDREHLKVGSGTVCQEDKHKRVGGTMEVVIVISDLLESTQHCSRSCNGKTEV
LYFDNFLPSEVPHLALSALKKIDWKKYGLILANVNDQDGHVFLEMDNFFSYVQIQIAL
HWYHNQYFTRQKNGPGISLLKKGIKNALDNLKAKHEGFILSSHSRKICSYVPDLARSI
AGLIFSSTDLDFQGDCLSVLGFGYGEVERDTVENYIQRKIVTVIGMNEKKPGKDQEAA
PFLFFDGESETSFFEDEEVEDDENSTHEYDATATKAYTQFKCLATMLQE"
                                                                                                                                                                                                                                                  /protein_id="AAB71970.1"
/db_xref="G1:2462751"
/db_xref="G1:2462751"
/translation="MAPEISVNPMYLSEKAHQAPPRRAYVTFLAGNGDYVKGVVGLAK
/translation="MAPEISVNPMYLSEKAHQAPPRRAYVTFLAGNGDYVKGVVGLAK
GLRKVKSAYPLVVAMLDDVPEBHREILLASQGCVVREIEPVYPDNQVEFAMAYYYLNY
SKLRIMNFEEYSKMIYLDADIQVFDNIDHLFDLSDAYFYAVMDCFCEKTWSHSLQYSI
complement(join(8347. .8443,8539. .8657,8941. .9066))
/gene="F8A5.3"
                                                                                                                                                                                           GYCQQCPEKVTWPEDMESPPPPLYFNAGMFVFEPSPLTYESLLQTLEITPPSPFAEQD
FLNWFFEKVYKPIPLVYNLVLAMLWRHPENVELEKVKVVHYCAAGSKPWRYTGEEANM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F8A5.2"
complement(join(3171. .3389,3471. .3605,3706. .4029,
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1845. .2159,2256. .2526,2788.
/gene="F885.1"
/note="Hypothetical protein"
                                                                                            complement(8347. .9066)
                                                                                                                                                                DREDIKMLYDKWWDYYNDESLDFKSKIPADAEETYTKSSILASYLEPEMTYFPAPSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="nearly identical to
protein gp|D26537|537404"
                                                                /gene="F8A5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="F8A5.1"
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/db_xref="taxon:3702"
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VWDVSCGKTEGLIGGATVLLENSKAQNKSGKQKLRLWQGKEADGSFPTSTPGKVPRHE
RGELERLEKLMNKYERGQIQSIDWLDRLMLKSLDTIKEQESTRIGSSHLETVVIDFCSF
EHRVVFQESGANLEITAPIGSTNEFTVFWDTELGKTWSSENKGKSLKSTIDRD
LKPSNIERKSIQRVLKYPPTRTLSGDERQLLWKFRFSUMSERRALTKFLRCVEWSDVQ
EAKQAIQLMYKWEMIDVCDALELLSPLFESEEVRAXAVSLERADDEELQCYLLQLVQ
ALREERSDRSCLSGFLVQRALQNIELASFLRHYVAVELHDHVYAKKFYSTYELLEENI
IKLPPGVNGEDGYQLWQSLVRQTELTAQLCSITREVRWYRGYTQKKEKRACHLEENI
IKLPPGVNGEDGYQLWQSLVRQTELTAQLCSITREVRWYRGYTQKKEKRLRQLLGGLL
SELTYFEEPIRSPLFPWLIKGIVAGESSLFKSALHELRLFRFFEFEEGGSCKLIFKKG
DDLRQDQLVVQMVWLMDRLKKLENLDLCLTFYKVLATGHDEGMLEFIFSRSLAQILSE
HRSITSLOKFHEDEHAPFGITATCLDTFIKSCAGYSVITYIIGIGGRLDMLLTIDD
GRLFHVDFAFILGADFREFPPMKLCKEMVEAMGGAESQYYTRFKSYCCEAXNILARS
SNLILNLFHLMAGSTIPDIASDPEKGILKLQEKFRLDMDDEACIHFFQDLINESVSAL
FPQNYETIHRWAQVWR"

15572. 17812
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//gene="F8655.4"
/note="location of EST gb|W43464"
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CESIRMSKKVDKTGQRTLAVVTKADMAPEĞLLQKVTADDVSIVLĞYVCVRNRIGETIY
EEARMQEELIKETIPVLSLIDEDIYGIPVLAĞKLMLIQSSMIARCLPKINGKLEV
EEARMQEELIKLEMVRASTGEALMALMDIIGSAKESLLRILVQGDESEYPDDINMKCTARL
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ADMLSQFSDSLQAKPKEVAEFLMDEIKILDECKUGLFNFIPRSAFLAILSQHVDGIQ
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join(15572. .16004,16236. .17812)
/gene="F8A5.5"
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NSRPVNGQPENIYEQISGMIMKYIEPQESIILNVLSATKPHWRRAYEQARMQEELLER
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EKPKEVTEFLMNEIKILDECKCVGLPNFIPRSAFLANLSQHEDAIHVKPVEFIKKIWD
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YHAHLLIPAFDMKMRITSYWKIVLRRIVDNLALYLQLSVKSLVNTREQKEIVAEMVDP
RDGGGVEKMLEESPLVASKREKLQNSIKLLKESKDAVAAIVDQNC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to "Mx" GTP-binding proteins"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(18712. .19150,19685. .19839,19981. .20987,21054. .21188,
21973. .20091,22335. .22510)
/gene="TRA5.6"
/note="similar to "Mx" GTP-binding proteins"
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                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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/db_xref="GI:2462737"
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hes 494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGCTTAGATCTGCCACCAATCATTTCAACTCGAAGAACATTCTCGGAAGAGGCGGATAC 108971
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                                                                                                                                                                                                                   acctacatgatcactgcgatccgaagatcattcaccgtgacgtaaaagcagcaaacatcc
                                                                                                                                                                                                                                                                                                                    ctccgcttgattggccaacgcggaagagaatcgcgctaggctcagctcgaggtttgtctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cttgtgtatccttacatggccaatggaagtgttgcttcgtgtctcagaggtaaaaactaa 3657
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ATAGAGACTCTCATGTCACAACTGCAGTCCGTGGAACTGTTGGCCCACATTGCACCTGAGT
                         ataaagacactcacgtgacaacagcagtccgtggcaccatcggtcacatcgctccagaat 4017
                                                                                                                     tottagacgaagaattogaagoggttgttggagattttogggttggcaaagottaatggact
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                                                                                         TGTTAGATGAGGACTTCGAAGCAGTTGTTGGTGATTTTGGGTTAGCTAAGCTTCTAGACC
                                                                                                                                                                                       ACCTACACGAGCAATGTGACCCGAAGATTATACACCGCGATGTGAAAAGCAGCTAACATTC
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/db_xref="G1:2462738"
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LQRSSSPEPEIWLEYSDKVVPTDEEHVABAICAATURDFLAGGSVSDTPLTLSVKKNI
VPDLTMYDLPGJTRVPVMGQPENIYEQISRMLIKKYIEPDESIILNVLSARVDFTTCES
IRMSRQVDKTGERTLAVVTKADMAPEGLLQKVTADDVSIGLGYICVRNRIGEETYEEA
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join(23787. .24210,24676. .25157)

join(23787. .24210,24676. .25157)
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Pred. No. 2.3e-45;
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              cgagtgatgggtttagtaacaagaacattttgggcagaggtgggtttggggaaagtctaca 3430
                                                                           CAACAAGCAATTTTAGTCCAAAGAACATTTTGGGACAAGGAGGGTTTGGGATGGTTTATA 72060
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                                                                                                                    AAGGGTATCTCCCAAATGGAACTGTGGTGGCAGTTAAAAAGATTGA---AAGATCCGATTT 72003
                                                                                                                                                                                                                                                                                                      484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-MAR-1998) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3934)
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/strain="Columbia"
/db_xref="taxon:3702"
/chromosome="5"
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/clone_lib="Mitsui P1"
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Pred. No. 4.1e-43;
0; Mismatches 252;
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eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-MAY-1998) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory Gene Structure 2, 1532-3, Yana Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
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                                                aatggactataaagacactcacgtgacaacagcagtccgtggcaccatcggtcacatcgc
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                                                ORGANISM
                                                                                           Daucus carota s
complete cds.
U93048
U93048.1 GI:22
Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
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                                                                          ttatgggttcataattgttggttacactaatgacacagagagggccaccgtcacaacctcc
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                                                                                                                                                                                              TATATCCATACATGGCTAATGGAAGTGTTGCGTCGTGTTTAAG-------
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Schmidt,E.D., Guzzo,F., Toonen,M.A. and de Vries,S.C.
A leucine-rich repeat containing receptor-like kinase marks
plant cells competent to form embryos
Development 124 (10), 2049-2062 (1997)
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Schmidt, E.D.L., Guzz
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VRGTLGYIAPEYLSTGKSSEKTDVFGYGJMLLELITGQRAFDLARLANDDDVMLLDWV
KSLLKEKKLEMLVDPDLENNYLDTEVEQLIQVALLCTQGSPMERPKMSEVVRMLEGDG
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347 c 407 g 495 t
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/protein_id="AAB61708.1"
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Pred. No. 1.5e-41;
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tacaagtggcgagtgatgggtttagtaacaagaacattttgggcagaggtgggtttggga
                                                              cagccgaagaagatccagaagttcatctgggacagctcaagaggttttcttttgcgggagc 3361
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                                               CAGCTGAAGAGGACCCAGAAGTGCACCTTGGTCAACTGAAGAGGTTTTCTCTGCGAGAAT
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Sequence
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2 from Patent WO9743427.
                                                                                                                                                                                                                                                                                                                         /codon_start=1
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PGONGFTGAIAGGVAAGAALLFAAPAMAFAWRRRKRREHFFDVPAEEDPFUHGQLK
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94. .1755
                                                                                                                                                                                                                                     LAEKWDEWQKVEVIHQDVELAPHRTSEWILDSTDNLHAFELSGPR"
354 c 415 g 515 t
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VRGTLGYIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWV
KSLLKEKKLEMLVDPDLENNYIDTEVEQLIQVALLCTQGSPMERPKMSEVVRMLEGDG
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                                                                                                                                     6.6%;
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                                                                                                                   Score 270.8; DB 5;
Pred. No. 1.5e-41;
0; Mismatches 157;
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                                                                                                                               Nakamura, Y.
Structural Analysis of
Unpublished (1999)
2 (bases 1 to 84896)
                                                                                                                                                                                                                                                                                                     complete sequence. AB025639 AB025639.1 GI:4589 HTG.
                                    Nakamura,Y.

Direct Submission
Submitted (02-APR-1999) to the DDBJ/EMBL/GenBank databases.
Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory
Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan
(E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
Fax:+81-438-52-3934)
                                                                                                                                                                                                                    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Euphyylophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Brassicales; Brassicaceae;
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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/organism-"Arabidopsis
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TCGA
                                                                             ataaagacactcacgtgacaacagcagtccgtggcaccatcggtcacatcgctccagaat
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/db_xref="taxon:3702"
/chromosome="3"
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Pred. No. 2.4e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence.
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AC005170.2 GI:659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-DEC-1999) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence versions of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana chromosome II section 135 of 255 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin,X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402 (6763), 761-768 (1999)
                                                                                                                                                                                                                                                                            like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                        F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would
                                                                                                       Address all correspondence to:
                                                                                                                                                               This work was supported by the National Science Foundation, 
Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                              We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
                                                                                                                                                                                                                                              database support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ittp://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to the bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 110211)
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/cultivar-"Columbia"
                                                                            Location/Qualifiers
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                                                       .110211
                                                                                                          at@tigr.org
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8152. .8268
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8152. .826
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complement(4565...4612)
/rpt_family="(CAA)n"
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complement(3570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"mfllillvecityfafvytnkgageaiegkgykeyklgdystwl
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ivflyflilyysvgccafrnnkrddsysrtygykp"
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/protein_id="AAF18611.1"
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15853. .15918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDPESIADHMYRMGLMALISSDIPGVNRDKCMKMAIVHDIAEAIVGDITPSCGISKEE
KNRRESEALEHMCKLLGGGERAKEIAELMREYEENSSPEAKVVKDFDKVELILQALEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKNVNRVFFCKSLSLVFLVPSFTRSHIRFTYSAAGASSPNRAIH
CMASDSPQSGDGSVSSPPNVAAVPSSSSSSSASSAIDFLSLCTRLKTTPRAGWIKRDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="(CAAAA)n"
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                                                                               /rpt_family=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="At2g23830"
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9582,9709.
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Best Local Similarity
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             gtaacaagaacattttgggcagaggttgggtttgggaaagtctacaagggacgcttggcag 3445
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                                                                                                        GTTCCAAGAGTATTCTTGGTGCTGGTGGGTTTGGTAATGTCTACAGAGGAAAATTCGGGG
                                                                                                                                                                                                                      Conservative
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CFRGLVLDISYRPVNVVCWKRAICLEYMDKADVLEYYDQTVSSPTGSFYIPAVLRVPH
LLQVVKRRRVKNSLSKKNILLRDDYTCQ"
                                                                                                                                                                                                                                                                                                                                                                        /pseudo
31472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(29076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unknown protein"
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                                                                                                                                                                                                                                6.2%;
58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          family-"POLY_A"
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                                                                                                                                                                                                                   Score 252.4; DB 50;
Pred. No. 2.5e-38;
D; M1smatches 316;
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                                                                                                                   Sato, S., Kotani, H., Nakamura, Y., Kaneko, T., Asamizu, E., Fukar Miyajima, N. and Tabata, S.
Structural analysis of Arabidopsis thaliana chromosome 5. I.
Sequence features of the 1.6 Mb regions covered by twenty physically assigned Pl clones physically assigned Pl clones DNA Res. 4 (3), 215-230 (1997)
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Direct Submission
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                              TCTCTGCACAGGAAAATCATCTGAAAAAACCGATGTTTTTGGTTACGGTATAACGCTTCT
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/strain="Columbia"
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Isseeds - useful in plant breeding [133p; English. 20ding SERK, a putative receptor kinase of a method of producing apomictic seed raining plant material with a nucleotide rain which in active form in a cell or ne cell embryogenic; (b) regenerating linto plants or carpel-containing the region of the religious containing the second of the religious processing the religious processi	idt EDL, Van Holst GJ;															ains introns"		lifiers		pomictic; seeds; production;		· .	ALIGNMENTS		X20248_08 Q47060			
ng r kinase. rr kinase. rtic seeds leotide cell or cating rating																				n; embryos;				O. longistaminata Staphylococcus aur	Continuation (9 of zmFK1 homologue pr	CF-5 pathogen resi CF-5 pathogen resi	Borrelia burgdorfe CF-5 pathogen resi	Plasmodium var-7 g Borrelia burgdorfe

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Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
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Best Local Similarity 100.0%;
Matches 4081; Conservative 0
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| cccgttgagatctttaaaaatattaaataatatatcaacgaaaaagctattttattcata
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	2880	2821 cotggatotococogtittotocotocacototttattoaacotococoagtitocaco	Qy 2
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	2820	1761 toottytycayttttyctaataacttayacotatytyyacotyttacaaytcacccatyt	Qу 2
	2820		Db 2
	2760	2701 atcctcttcagttatttcagttgttgtgtcagtgtctgaacttattctgaaactttcatt	Qy 27
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	2700)641 tggttcagttcctgacaatggctccttctcactcttcacaccccatcaggttctatgattt	Qy 2
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	2580)521 tgtgagtoctotoattaactttoatttatgtotacttoattotocotoagttgatttgtt	Qy 2:
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	2520 2520	#61 acaacagtctcactgggtcaattcctatgtcactgaccaatattactacccttcaagtgt 	Db 2
	2460 2460	401 tttgttccaatttttgactctttgctgaaaattttacatgcaagaatagccggcttaaca 	Db 2
	2400	3341 atttetgtgagtatacatatgetttaeeggeteagttaeagtetttgtttaatettaggt	Qy 2:
	2400		Db 2:
	2340	281 ttacttaaacagcttctccggtcctattccggaatcattgggaaagctttcaaagctgag	Qy 2:
	2340		Db 2:
	2280	1221 cataactggcccgattcctagtaatcttggaaatctgacaaacttagtgagtttggatct	Qy 2:
	2280		Db 2:
	2220	1161 tgtaattgaaatctttttaacaagtttcttattttcttacagggaggtttacagtaacaa	Qy 2:
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	2100	041 ccatttagttccagagcttggtgtgctcaagaatttgcagtatttgtaagttccacttat	Оу 2(
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	2040	981 taccgacatttttgtttctttttgtcaaatacagtgatttggggaatgcagagttatctgg 	Db 15
.,	1980 1980	921 ataagagtgtaaagctttcttctactaatcccactttttaaactttgacctcagcgtggt 	Dy 19

y 3961 aagacactcacgtgacaacagca 	41 tacatgatcactgcgat	Db 3721 TTTATGGGTTCATAATT Db 3721 TTTATGGGTTCATAATT Oy 3781 cgcttgattggccaacg	3661 attaaacatct	Oy 3541 gttcatcgaaa Db 3541 GTTCATCGAAA Oy 3601 gtgtatcctta Db 3601 GTGTATCCTTA	3481 gagcgaac 3481 GAGCGAAC	Qy 3361 ctacaagt	3301 gca 3301 gca	y 3241 ag	Qy 3181 gccagc	Qy 3121 actaga Db 3121 ACTAGA	Qy 3061 tgctgc Db 3061 TGCTGC	Qy 3001 taatti
961 aagacactcacgtgacaacagca 	841 tacatgatcactgcgat	721 TTTATGGGTTC 721 TTTATGGGTTC 781 cgcttgattgg: 781 CGCTTGATTGG	661 attaaacatcti 661 aTTAAACATCT	541 gttcatcg 541 GTTCATCG 601 gtgtatcg 601 GTGTATCG	.481 gagcgaac .481 GAGCGAAC	361 ctacaa 361 CTACAA 421 aaagtc 421 AAAGTC	301 gca	241 agt	181 gccag 181 GCCAG	121 actag 121 ACTAG	061 tgctg 061 TGCTG	001 taatt
gacactczcgtgacaacagca 	acatgatcactgcgat	TIATGGGTTC: TTATGGGTTC: gcttgattgg:	ttaaacatcti TTAAACATCT	ttcatcg	cgaac CGAAC	caa CAA	5-5	9-6	ccag CCAG	ctag CTAG	gctg 	taatti
tccgtggcaccatcggtcacatcgctccagaatatc 4	CCGAAGATCATTCGCGGTTGGCAAAGCTAATGGACTATA 396	CCCCGAAGAATCCCCTAACCCTCAACCCCAACCTCAACCTCAACCCCAACCCCAACCCCAACCAACCTCAATGACACAGAGAGAG	teteteaattaetttgaegtgaagtgtttttteatgttttee 37	acctgttgagattacgaggtttctgtatgacacgaacgatggct 360	aggtggagagctccagtttcaaacagaagtagagatgataagtatgg 	tggcgagtgatgggtttagtaacaagaacattttgggcagaggtgggtttggg 342 [agaagatccagaagttcatctgggacagctcaagaggttttctttgcgggag 33 	gttttttaagttacaaactcttttgagtaaaatctcgattgcaaaatctctat 3 	aattttgttttgcagaaaagtattggaacaactgttaatgaaaatcaatacata 324 	tattttottogatgtgootggtgagtttattattogcattagtttotgttotta 318 	Ctttgctctttgctgctcctgcaatagcctttgcttggtggcgacgaagaaagcc 312 	tgatttcaggtgggtatggtataactggagcaatagctggtggagttgctgcagg 306

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Cit has be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.;
Best Local Similarity 85.;
Matches 664; Conservative
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V06591;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK gene.
receptor kinase; apomixis; apomi
plant breeding; ds.
Arabidopsis thaliana.
Key
Location/Qualifi
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20-N0V-1997; E02443;
13-MAY-1996; GB-010044.
[NOVS] NOVARTIS AG.
[NOVS] NOVARTIS AG.
De Vries SC, Hecht VFG, $
WPI; 98-08529/08.
P-PSDB; W47023.
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/product= SERK protein
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                                                                                   intron
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5295. .5803
/*tag= 1
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/number= 5
4642. .4757
/*tag= g
/number= 6
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                               /number= 8 6197. .6339
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                                                                                                                                                                                                                                                       gcttgattggccaacgcggaagagaatcgcgcttaggctcagctcgaggtttgtcttacct
CTCAACCGGAAAATCTTCAGAGAAAACCGACGTTTTCGGATACGGAATCATGCTTCTAGA
                                                                                                                                                                              ACATGATCACTGCGATCCGAAGATCATTCACCGTGACGTAAAAGCAGCAAACATCCTCTT
                                                                                                                                                                                                                                        GCTTGATTGGCCAACGCGGAAGAGAATCGCGCTAGGCTCAGCTCGAGGTTTGTCTTACCT
                                                                                                                                                                                                                                                                                                                ttatgggttcataattgttggttacactaatgacacagagaggccaccgtcacaacctcc
                                                                                                                                                                                                                                                                                                                                                                                     ttaaacatcttgtgctctctctcaattactttgacgtgaagtgtttttcatgttttcct
                                                                                                                                                                                                                                                                                                  AGAGAGGCCACCGTCACAACCTCC
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tor kinase; apomixis; breeding; ds. (first entry) /*tag= c /nnumber= 2 4124. .4211 /note= "contains introns" 3731. .3802 /*tag= b /number= 3851. .39 ocation/Qualifiers DNA; /*tag= .3979 6695 apomictic; ΗP seeds; production; embryos;

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plant parts; and (c) expressing the sequence in the vicinity
of the embryo sac. The apomictic seeds and embryos thus produced
can be developed into plant progeny. This is useful in plant
breeding programs. Controllable and reproducible apomixis provides
many advantages in plant improvement and cultivar development in
the case that sexual plants are available as crosses with the
propagated hybrids and could shorten and simplify the breeding
propagated hybrids and could shorten and simplify the breeding
process so that selfing and progeny testing to produce and/or
stabilise a desirable gene combination could be eliminated.
Apomixis allows plant breeders to develop cultivars with
specific stable traits for such characteristics as height,
seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 903; Conserv
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20-NOV-1997.
13-MAY-1997; E
14-MAY-1996; C
(NOVS) NOVART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of apomictic seeds - useful in plant breeding Claim 21; Pages 40-46; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4094
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De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

WPI; 98-086529/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTACTGGATAGGCGTCTCAACAACAACTGCTCTCTGGTCCAATTCCAATGTCACTGA
                                                                                                                                                                                                                                                                                                                                                                      catgcaagaatagccggcttaacaacaacagtctcactgggtcaattcctatgtcactga 2496
                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgaacttattctgaaactttcatttc--
                                                                                                                                                                                                                       CTAATATTACAACTCTTCAAGTCCTGTAAGTATTCCGACCTTTCCAGATAGTT-----
                                                                                                                                                                                                                                                                                              TICACTAGTITITAACTIAAIGCAATIIGATIAICCTTICAAGIGAIIGATIAIAICACA 4198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTAGGAAAGCTTACAAGGCTAAGATTCTTGTATGACTACAAAT------C
                                       TACACCTATCAGGTTTAATGCTAGTAATATCTTTAATATTATGGTTCTTACTTCTACTGC
                                                              903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 506;
-----cttgtgcagttttgctaa
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	5398 G 5398	닭
	3741 g 3741	Qy
3740 5397	3681 totcaattactttgacgtgaagtgttttttcatgttttcctttatgggttcataattgtt	Db 69
33 6		D 4
52 77	CTACGTGGTTTCTGCATGACACCTACCGAGCGGCTTCTTGTATATCCCATACATGGCT	o B
3620	acgaggittctgtatgacaccgaccgag	Qy
5217	5001 YCLCGYCLCGGGCGYGGYGGYGGGGGGGGGGGGGGGGGG	B 8
1 5	098 TGCTGATGGCTCACTTGTAGCAGTTAAAAGGCTTAAAGAACGAAC	용
3500	ctcttgttgctgtcaagagactgaaggaagagcgaactccaggtggaga	Qy
5097	Soet Clean Carea Seet Carea B &	
04	984 AGTGCACCTTGGTCAACTGAAGAGGTTTTCTCTGCGAGAATTGCAAGTCGCAACGGATAC) B
38	321 agttcatct9ggacagctcaagaggttttctttgcgggagctacaagtggcgagtgatgg	V Q
4983	CTGTCTGTGGACTTTGTTTCACTGTCATTAGTTAACTTCAGCTGAAGAGGACCCAGA	Дb
3320		Qy
4923	TATTGAAGCGCT	망
3260	ttaagtta	VΩ
4910	GGTTAGTCCTGTAAATAGATA	멍
3200	gcctggtgagtttattattcgcattagtttctgttcttagccagcaattttgttttgca	γQ
4883		Дb
3140	tcctgcaatagcctttgcttggtggcgacgaagaaagccactagatattttcttcgatg	Qy
4823	4764 ATGGTCCCACTGGAGCTATTGCTGGGGGAGTAGCTGCTGGTGCTGCTTTACTGTTTGCTG	멍
3080	ggtataactggagcaatagctggtggagttgctgcaggtgctgctttgctctttgctg	Qγ
4763	TTCTTTCTCTTCTTATTATGAAGGACAAA	В
3020	tataactcatcttgccaataaggcaataaccaaatgatctaatttgatttcaggtgggt	Qy
4717	CCCGTAATTAATTTTATGACTGTAAAAATTGGTGTTAATTTCACCAGTTGCGA	당
2960	yaaacagaagatgaaatetttgettetetgteaateettttete	Qy
4657	CAGCCTCCAGGTGATTTAGTTTTAT	ф
2900	cctccacceccttttattcaacctcccccagtttcccacccgagtaagcctcctcttt	Qy
4597	4538 TAATTTGAATTTATGTGGACCTGTAACTGGGAGGCCCTGCCCCTGGATCTCCCCCATTTTC	Дb
2840	aacttagacctatgtggacctgttacaagtcacccatgtcctggatctcccccgttttc	Qy
4537	4478 GAAAGCTATGATAATATTTTTTTTCTCCTTCATATATTATCACTTTCGCAGTTTTGGCAG	ర్థ

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CC The sequence is that encoding SERK, a putative receptor kinase. CC It may be used as part of a method of producing apomictic seeds CC comprising; (a) transforming plant material with a nucleotide cc sequence encoding a protein which in active form in a cell or CC cell membrane renders the cell embryogenic; (b) regenerating CC the transformed material into plants or carpel-containing CC plant parts; and (c) expressing the sequence in the vicinity CC of the embryo sac. The apomictic seeds and embryos thus produced CC can be developed into plant progeny. This is useful in plant CC the case that sexual plants are available as crosses with the CC many advantages in plant improvement and cultivar development in CC the case that sexual plants are available as crosses with the CC apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding corporates so that selfing and progeny testing to produce and/or CC stabilise a desirable gene combination could be eliminated. CC Apomixis allows plant breeders to develop cultivars with CC seed and forage quality and maturity.

SQ Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 504
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21-MAY-1997; E02443.
13-MAY-1996; GB-010044.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De VY-168 SC, Hecht VFG, 1981; 98-086529/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daucus carota SERK gene receptor kinase; apomix plant breeding; ss.
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03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V06571 standard;
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                                                                                             941
                                                                                                                                                           881
                                                                                                                                                                                                                       821
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                                                                                                                                                                                                                                                                                                                                              707
                                                                                                                                                                                                                                                                                                                                                                                                         Local Sinhes 504;
                                                                                                                                                                                                                                                                                                                                                              | cagccgaagaagatccagaagttcatctggggacagctcaagagggttttcttttgcgggagc
                                                                                                                                                                                                                                                                                                  agcgaactccaggtggagagctccagtttcaaacagaagtagagaggatgataagtatggcag
                                                                                                                                                                                                                                       TGCAAGTCGCAACGGATACTTTTAGT-----ACCATACTTGGAAGAGGTGGATTTGGTA
                                                                                                                                                                                                                                                                                                                                              CAGCTGAAGAGGACCCAGAAGTGCACCTTGGTCAACTGAAGAGGTTTTCTCTGCGAGAAT
                                                                                                                                                           AACGAACACCAGGTGGTGAGCTGCAGTTTCAAACAGAGGTGGAAATGATTAGCATGGCTG
ttaaacatcttgtgctctctctaattactttgacgtgaagtgttttttcatgttttcct
                                                tgtatccttacatggccaatggaagtgttgcttcgtgtctcagaggtaaaaactaaacaa
| ||||| ||||||||
                                                                                                                                                                                                                       AGGTGTATAAGGGACGCCTTGCTGATGGCTCACTTGTAGCAGTTAAAAGGCTTAAAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carota.
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apomixis; apomictic; seeds; production; embryos;
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                                                                                                                                                                                                                                                                                                                                                                                                                         64.68;
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                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                         Score 270.8; DB 1;
Pred. No. 7.6e-52;
0; Mismatches 157;

    useful in plant breeding

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gtcacaacctccgcttgattggccaacgcggaagagaatcgcgctaggctcagctcgagg TCTTCTGTTCTATGACTATTTGGAAAATGGTAGCCTCTGGGATCTTCTTCATGGCCCTAC Query Match
Best Local Similarity
Matches 207; Conserv

Conservative

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Score 108; DB Pred. No. 3.8e 0; Mismatches

108; DB 1; No. 3.8e-15;

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DNA encoding plant morphogenesis regulatory protein - useful tyleld plants with short stems or altered inflorescence I yield plants with short stems or altered inflorescence I yield plants with short stems or altered inflorescence I yield plants with short stems or altered inflorescence. The present sequence encodes an Arabidopsis thaliana plant comphogenesis regulatory protein (MRP), which can be used to I a plant with, e.g. short stems or altered inflorescence. The I cats on a plant at a specific site for a specific period, and I cats on a plant at a specific site for a specific period, and I cats on a plant at a specific site for a specific period, and I cats on a plant at a specific site for a specific period, and I cats on a plant at a specific site for a specific period, and I cats on a plant at a specific site for a specific period, and I cats on a plant to increase its MRP expression, and therefore control the plant to increase its MRP expression, and therefore control the sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;
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(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KEN (CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU WPI; 97-206629/19.
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUN-1997 (first entry)
Arabidopsis thaliana plant morphogenesis regulatory protein
Plant; morphogenesis; regulation; short; stem; alteration;
inflorescence; extraneous; gene; expression; transformation;
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T62124;
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Best Local S
Matches 186
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24-JUN-1997; US-881706.
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Chory J, L1 J;
WPI; 99-081275/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      morphogenesis regulatory protein (MRP), which can be used to yie a plant with, e.g., short stems or altered inflorescence. The MRF acts on a plant at a specific site for a specific period, and cat therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant. Sequence 9295 BP; 2873 A; 1581 C; 1602 G; 3239 T;
                                                                                                                                                           WO9859039-A1.
30-DEC-1998.
24-JUN-1998; C
24-JUN-1997; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding plant morphogenesis regulatory protein yield plants with short stems or altered inflorescence claim 6; pages 12-15; 17pp; Japanese.

The present sequence encodes an Arabidopsis thaliana
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New receptor kinase Binl involved in brassinolide signalling - useful for promoting increased yield and disease resistance in plants and for modulating occyte maturation Claim 8; Page 49-52; 72pp; English.
This DNA sequence codes for a novel plant steroid receptor kinase, designated Binl (see W97819), which is involved in the pathway for the synthesis of the plant steroid hormone, brassinolide. 18 New
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BIN1; steroid receptor; receptor kinase; transgenic
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86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to respond to brassimolide, and were named bin mutants. The binic mutations were used to map the gene to a small interval on Arabidopsis chromosome 4. Bini was cloned by map-based cloning. The Bini polynucleotide was identified within this interval by generally the wild-type and mutant alleles of this nucleic acid. Overexpression of Bini in transgenic plants over the plants of characterised as having enhanced disease resistance, increased plants of plant yield or vegetative biomass and increased seed yield. Expression of Bini may also increase resistance to pesticides. CC inhibition of Bini, e.g. using antisense oligonucleotides (AON), is cused to render plants male-sterile, and to reduce their stature or yield, e.g. for creating dwarf varieties. Since Bini homologues can be involved in regulation of the menstrual cycle and uterine compared to proving success of in vitro fertilisation and to prevent premature labour. Transgenic animals are also provided, and are models for studying steroid-receptor interactions or can be used to screen for therapeutic agents.

So Sequence 4104 BP; 1061 A; 870 C; 930 G; 1243 T;
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Best Local S
Matches 175
                                                                                                      Zea may:
W09908151-A2.
W09908151-A2.
25-FEB-1999.
17-JUL-1998.
U14841.
13-AUG-1997. US-910386.
(REGC ) UNIV CALIFORNIA.
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to respond 1
                New RRK polynucleotides and nucleic acid constructs generating transgenic plants resistant to Xanthomonas Claim 12; Page 58-59; 67pp; English.
This invention describes a method for conferring disea
                                                                                                                                                                                                                                                     17-JUN-1999 (first entry)
Maize Xa21 gene DT4 cDNA fragment.
                                                                                                                                                                                                                         plant
                                                                                                                                                                                                                                            Xa21;
                                                                                                                                                                                                                                                                                                       X23531 standard; cDNA;
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18-MAR-1999.
07-SEP-1998; J04010.
08-SEP-1997; JP-259235.
(RPRG-) RPR GENCELL ASIA F
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Sequence 3045 BP; 717 A; 739 C; 744 G; 735 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Base sequence of the plasmid pRx-ires-bsr.

Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nflammatory disease;
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Sequence 6644 BP; 2166 A; 1573 C; 1424 G; 1481 T;
                                                                                                                       25-JUN-1999 (first entry)
Base sequence of the plasmid pRx-Bcl-xl-bsr.
COWPOX virus; bsr; viral vector; expression; approximation; bcl-2; bcl-xl; FLIP; survivin; IAP; ILP; autoimmune disease; graft rejection reaction; inflammatory disease; ss.
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18-MAR-1999. 07-SEP-1998; Homo sapiens. W09913073-A2. Synthetic.

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Combined the present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. CC The recombinant viruses generated are capable of expressing apoptosis-sasociated genes. These can then be used in a variety of diseases for cc which the induction of apoptosis by gene transfer, or where the induction of apoptosis by gene transfer, or where the cancer cc therapy for destroying cancer cells selectively. The treatment of cautoimmune diseases and graft rejection reaction, and apoptosis induction ct therapy for inflammatory cells in inflammatory diseases. Prior arts have cencountered the problem where if an adenovirus vector capable of cxpressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of ct the required to induce cell death by apoptosis is shorter than that combined to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the cromation areample from the present the human Bcl-xl gene, and cc plasmid pRx-Bcl-xl-bsr, which contains the human Bcl-xl gene, and cc sequence 7372 BP; 2353 A; 1749 C; 1649 G; 1621 T;
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(RPRG-) RPR GENCELL ASIA PACIFIC Hamada H;
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                                                                                             tgtaaaggcatgttctttgggttgaaaagctgggttatttgatatcttaagattgatgtt
                                                                 291;
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Pred. No. 3
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                                                                                                                                                                                                                                               PT New applosis-resistant virus-sensitive cell
PS Example 1; Page 34-38; 51pp; English.

CC The present invention describes an apoptosis-resistant virus-sensitive
CC cell line into which an apoptosis resistance gene has been introduced.

CC The recombinant viruses generated are capable of expressing apoptosis-
CC associated genes. These can then be used in a variety of diseases for
CC which the induction of apoptosis by gene transfer, or where the
CC inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
CC are useful as vectors for gene therapy which can be applied to cancer
CC therapy for destroying cancer cells selectively, the treatment of
CC autoimmune diseases and graft rejection reaction, and apoptosis induction
CC therapy for inflammatory cells in inflammatory diseases. Prior arts have
CC expressing an apoptosis-associated gene is introduced into animal cells,
CC expressing an apoptosis-associated gene is introduced into animal cells,
CC time required to induce cell death by apoptosis is shorter than that
CC required to replicate and produce the virus, resulting in failure to
CC obtain a recombinant virus having the integrated apoptosis-associated
CC apoptosis resistant gene introduced) is established and overcomes the
CC apoptosis resistant gene introduced) is established and overcomes the
CC problem. The present sequence represent invention.

SQ Sequence 7797 BP; 2542 A; 1760 C; 1656 G; 1839 T;
                                                                                                                                                        Query Match
Best Local S
Matches 291
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07-SEP-1998; J04010.
08-SEP-1997; JP-259235.
(RPRG-) RPR GENCELL ASIA F
Hamada H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1999 (first entry)
Cowpox virus bsr full length gene sequence.
Cowpox virus; bsr; viral vector; expression; apoptosis; resistance;
Compox vbrus; bsr, viral vector; expression; apoptosis; resistance;
crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer;
autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4479 TTTTTTTTTTTTGCAACTGCAAGAGGGTTTATTGGATA
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hes 291;
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Pred. No. 3.3e-09;
0; Mismatches 348;
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IN X33184/c
ID X33184/c
ID X33184/c
ID X3318
AC X331
DT 25-J
DE Base
KW CrmAb
KW auto
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                                                                                                                                  Provided the problem where if an adenovirus vector capable of expressing an apoptosis resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The present invention describes an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis associated genes. These can then be used in a variety of diseases for conhibition of harmful apoptosis by gene transfer, or where the cinhibition of harmful apoptosis, is therapeutic. The recombinant viruses care useful as vectors for gene therapy which can be applied to cancer through for destroying cancer cells selectively, the treatment of care useful as vectors for gene therapy which can be applied to cancer therapy for inflammatory cells in inflammatory diseases. Prior arts have cencountered the problem where if an adenovirus vector capable of capacities producing the virus will be destroyed because the period of the cells producing the virus will be destroyed because the period of contain a recombinant virus having the integrated apoptosis associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant yene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the cell sused in an example from the present invention.

Sequence 7996 BP; 2463 A; 2015 C; 1829 G; 1689 T;
   Query Match
Best Local Similarity
Matches 291; Conserv
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07-SEP-1998; J04010.
08-SEP-1997; JP-259235
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WPI; 99-204431/17.
P-PSDB; W23533.
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This invention describes a method for conferring disease resistance in plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins can be used for enhancing resistance to Xanthomonas in a plant, preferably in
                                                              New RRK polynucleotides and nucleic acid constructs - generating transgenic plants resistant to Xanthomonas Claim 14; Page 61-62; 67pp; English.
This invention describes a method for conferring disearch
                                                                                                                                                                                                                                     17-JUN-1999 (first entry)
Tomato Xa21 clone TRK2 DNA fragment.
Xa21; receptor kinase-like protein; plant disease resistance; cassava; m
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13-AUG-1997; US-910386.
(REGC) UNIV CALIFORNIA.
Hulbert SH, Richter T, R
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cassava; maize; tomato; Xanthomonas; ss.
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Best Local Similarity 54.0%;
Matches 161; Conservative
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20-NCV-1997:
13-MAY-1997: E02443.
14-MAY-1996: GB-010044.
14-MAY-1996: GB-010044.
10-VI S SC, Hecht VFG, Schmidt EDL, V&WPI; 98-086529/08.
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                                                                                                                                                                                                            Production of apomictic seeds - useful in plant breeding Claim 28; Pages 75-77; 123pp; English.
The sequence is that of an EST clone showing high homology SERK LRR (leucine-rich repeat) sequences.
Sequence 981 BP; 286 A; 236 C; 180 G; 279 T;
                                                                                                                                                                                                                                                                                                                                                                                                                            V06587 standard; cDNA to mRNA; 981 BP. V06587; 03-AUG-1998 (first entry) Arabidopsis thaliana SERK LRR homologous receptor kinase; apomixis; apomictic; see plant breeding; leucine-rich repeat; ss. Arabidopsis thaliana.
                                                                                                              1794 aggtgatgctttgcatactttgagggttactctagttgatccaaaccaatgtcttgcagag 1853
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                      cagtgtcataagagtgta
                                                 CTGGGATCCAACTCTTGTTAATCCTTGTACCTGGTTCCATGTCACCTGTAACCAAGACAA
                                                                                                  AGGAGATGCTCTACGCTCTTCGCCGGAGTTTGACAGATCCAGACCATGTCCTCCAGAG
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; Pred. No. 1.5e-
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; Pred. No. 2.5e
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Search completed: June 23, Job time: 40529 sec
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03-AUG-1998 (first entry)
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous ES
receptor kinase; apomixis; apomictic; seeds
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Arabidopsis thaliana.
Cocation/Qualifiers
CDS
142. .798
                                                                                                                                                                                                                                                                                                                       W09743427-A1.
20-NCV-1997;
13-MAY-1996; GB-010044.
14-MAX-1996; GB-010044.
(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG, Schmidt EDL, Va
WPI; 98-086529/08.
P-PSDB; W47018.
                                                                                                                                                                                                                                                              Production of apomictic seeds - useful in plant breeding Claim 28; Pages 71-73; 123pp; English.
The sequence is that of an EST clone showing high homology SERK LER (Leucine-rich repeat) sequences.
Sequence 1106 BP; 331 A; 258 C; 206 G; 311 T;
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                                                                             1914 cagtgtcataagagtgta 1931
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production; embryos;
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Match
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/6_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-447-185-2
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US-07-717-331F-4
US-08-487-626B-13
US-08-628-417-6
US-08-628-417-6
US-08-587-680A-3
US-08-587-680A-1
US-08-587-680A-1
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US-08-587-375-1
US-09-014-369-14
US-09-014-368-13
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US-08-487-826B-13
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Patent No. 5670367
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Sequence 1, Appli	Sequence 29, App.	Sequence 15, App.	Sequence 5, Appl:	Sequence 15, App.	Sequence 1, Appl:	Sequence 9, Appl:	Sequence 13, Appl	Sequence 3, Appli	Sequence 24, Appl	Sequence 24, Appl	Sequence 3, Appli	Sequence 12, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 20, Appl	Sequence 18, Appl	Sequence 1, Appli

ALIGNMENTS

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; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                     TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7216 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: VA
COUNTRY: USA
ZIP: 22313-0299
ZOMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: PACETIME PC COMPOTERS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: DORNER, F.

APPLICANT: SCHEIFLINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/935
APPLICATION NUMBER: US/07/935
FILING DATE: 26-AUG-1991
ATTORNEY_AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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FILING DATE:
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Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                         APPLICATION NUMBER: US/08/587,680A FILING DATE: 17-JAN-1996
                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
APPLICATION NUMBER:
                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggttcagttcctgacaatggctccttctcactcttcacacccatcaggttctatgattta 2701
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Song, Wen-Yuang
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US 60/004,645
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 165; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                      TITLE OF INVENTION: Plant Clavatal Nucleic & TITLE OF INVENTION: Transformed Plants, and NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                APPLICANT: Meyerowitz, Elliot | APPLICANT: Clark, Steven E. APPLICANT: Williams, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1282 GA 1283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pair
                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                    COUNTRY:
                                                                                                                                           STATE:
                                                                                                                                                            CITY: San Francisco
                                                                                                                                                                             ADDRESSEE: Flehr, Hohbach, STREET: Four Embarcadero C
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                                                                                                                                           California
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(415) 576-0300
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                                                                                                                    United States
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Pred. No. 1.2e-08;
0; Mismatches 134
                                                                                                                                                                                 Albritton & Herbert
Suite 3400
    Version #1.30
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; LOCATION:
US-08-473-553A-1
                                                                                                                                                                                                                                                                                        RESULT 4
US-08-447-185-2
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                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Tanksley,
APPLICANT: Martin, G
TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity 53.6
Matches 133; Conservative
                                                                                                                                                                                                                                       Sequence 2, Application US/08447185
Patent No. 5648599
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4793 AAGGTGGTCATCTTCAATGGGAGACGAGACATAGAGTAGCCGTGGAAGCTGCAAAGGGCT 4852
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                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                          3952
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LOCATION:
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REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
                                                                                                 STREET:
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                                                               COUNTRY:
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                                                    14603
                                                                                                 Rochester
                                                                                New York
                                                              U.S.A.
                                                                                                                                                                    Tanksley, Steven D.
Martin, Gregory B.
MENTION: GENE CONFERRING DISEASE RESISTANCE
VENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PATHOGI
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Pred. No. 1.8e-06;
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US-08-447-185-3
Sequence 3, Application US/08447185
Patent No. 5648599
GENERAL INFORMATION:
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Best Local Similarity 53.4%;
Matches 149; Conservative
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                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            APPLICANT: Tanksley, Steven D.
APPLICANT: MARTIN, GENEGORY B.
TITLE OF INVENTION: GENE CONFERRING DISEASE RESISTANCE
TITLE OF INVENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PATH
NUMBER OF SEQUENCES: 5
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CURRENT APPLICATION DATA:
               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263
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STRANDEDNESS: double
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SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                             CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                   STREET:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccgagagattgcttgtgtatccttacatggccaatggaa 3625
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                                                                                                                                                                                          New York
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                                                                                                                                                                                                                                   Clinton Square, P.O. Box 1051
                                                                                                                                                                   U.S.A.
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                                                                                                                                                                                                                                                        Michael L. Goldman
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US/08/447,185
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Pred. No. 8.1e-06;
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NAME: GOLDMAN MT., MICHAEL L.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1000
TELEPAX: (716)-263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2443 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/07717331F Patent No. 5484905 GENERAL INFORMATION:
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Best Local Similarity 53.4%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                APPLICANT: June Nasr
APPLICANT: Stein
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic)
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APPLICATION NUMBER: US/08/111,078
                                                                                                                                                                                                                                  STREET: __
STREET: __
Trumbull
ATTORNEY/AGENT INFORMATION:
                                                                        COMPUTER: MACLILL MS-DUS
OPERATING SYSTEM: MS-DUS
OPERATING SYSTEM: MS-DUS
OPERATING SYSTEM: MS-DUS
OPERATING DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 ATGAGATGATTCTAATTTATAAATACATGGAGAATGGGA 424
                    APPLICATION NUMBER: US/07/717,331F FILING DATE: June 19th 1991 CLASSIFICATION: 800
                                                                                                                                                                                              COUNTRY: C
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                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                    Connecticut
                                                                                                                                                                                                                                                                      25 Skytop Drive
                                                                                                                                                                                                                  USA
                                                                                                                                    Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                          June Nasrallah; Michael Nasrallah; and Joshua
                                                                                                                                                                                                                                                                                          Yahwak & Associates
                                                                                                                                                                                                                                                                                                                                                  A Receptor Protein Kinase Gene
Encoded At The Self-Incompatability Locus
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Pred. No. 1.3e-05;
0; Mismatches 127;
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 9:
              COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTOREY/AGENT INFORMATION:
NAME: GEOIGE M. YANWAK
REGISTRATION NUMBER: 26,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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LENGTH: 2571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
07-717-331F-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3778 ctccgcttgattggccaacgcggaagagaatcgcgctaggctcagctcgaggttttgtctt 3837
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein TITLE OF INVENTION: A Receptor Protein Kinase Gene TITLE OF INVENTION: Encoded At The Self-Incompatability I NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
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STREET: 7-nnect
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25 Skytop Drive
                                                                                                                                                                                                                                                                              USA
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Pred. No. 2.1e-05;
0; Mismatches 145;
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TELEPHONE:

(203)268-1951

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US-07-717-331F-4
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2833 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/07717331F Patent No. 5484905
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Best Local Similarity
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717,331F
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION INFORMATION:
TELEPHONE: (203)268-1951
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At The Self-Incompatability Locus
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Yahwak & Associates
STREET: 25 Skytop Drive
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                                                                                                                                                                                                                                                                                                                       SIREET: 20
CTTY: Trumbull
                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                        USA
(203)268-1951
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Pred. No. 2.2e-05;
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; STRANDEDNESS: single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
US-07-717-331F-4
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Best Local S
Matches 141
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Patent No. 582109
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                               FILING DATE:
APPLICATION NUMBER: US 07/847,564
ETLING DATE: 03-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pochopien Ph.D., Donald J.
REGISTRATION NUMBER: 32,167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: U.S.
STREET: U.S.
CITY: Chicago
CITY: Illinois
TISA
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                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1672 GAAATTGCAGTGAAGAGACTATCGGAAATGTCAGCTCAAGGTACCGATG---AGTTCATG 1728
                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rothstein, Steven J.
APPLICANT: Goring, Daphne
TITLE OF INVENTION: S-LOCUS REC
TITLE OF INVENTION: SELF-INCOMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity hes 141; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTCATCTCTTTGATGAAACCAGAA 1873
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                   312-707-9155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-LOCUS RECEPTOR KINASE GENE IN A SELF-INCOMPATIBLE BRASSICA NAPUS LINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                             US/07/959,945
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Pred. No. 0.00017;
0; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malloy, Ltd
Suite 3400
                                                                                                                                                                                                                                                                                                                Version
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US-08-487-826B-13/c
                                                                                                                                                                                                                                   Sequence 13, Application US/08487826B Patent No. 5993827 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.3%;
Best Local Similarity 50.8%;
    APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.

APPLICANT: Miller, Louis H.

APPLICANT: Peterson, David S.

APPLICANT: Su, xin zhaun
APPLICANT: Su, xin zhaun
APPLICANT: Wellems, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: BIND PLASMODIUM FALCIPARUM ERVIHROCYTE BINDING PROTEINS
TITLE OF SEOUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS

LOCATION: 1..2574

LOCATION INFORMATION:

PUBLICATION INFORMATION:

AUTHORS: GORING, DAPHNE

AUTHORS: ROTHSTEIN, STEVEN J.

TITLE: ROTHSTEIN, STEVEN J.

TITLE: S-LOCUS RECEPTOR KINASE GENE IN A

TITLE: FUNCTIONAL SERINE/THREONINE KINASE

RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3838 acctacatgatcactgcgatccgaagatcattcaccgtgacgtaaaagcagcaaacatcc 3897
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LENGTH: 2749 base pairs
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STRAIN: oleifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                           TTCTTGA 2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTACGCAATGGATGGGGTATTCTCGGAAAAAATCAGATGTTTTCAGTTTTTGGAGTCATTG 2161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGACGAGACTGAAGCTAACACAAGGAAGGTGGTCGGAACTTACGGCTACATGTCTCCGG
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Newport Center Drive
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Pred. No. 0.00034;
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Bear
16th
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RESULT 11
US-08-628-417-6/c
US-08-628-417-6/c
; Sequence 6, Application US/086284;
; Patent NO. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITO!
; TITLE OF INVENTION: POLYMERAS!

US/08628417

COMPETITOR PRIMER ASYMMETRIC POLYMERASE CHAIN REACTION

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TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.3%;
Best Local Similarity 48.1%;
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08,
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                  15545
15425 CTTTTTTAATATAA 15412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   1396 actogriticicaattactitcicgatictittitattiggaggigaatcgctatctitag 1455
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                         1696 agcctctaatctca 1709
                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Israelsen, Ned REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                  tgtotgoattttgatttatgaaaattgttgttgttotttgtatttgtaagatttagtggc 1515
                                                                                                                                                                                          tagtactttgaatacactgttttgcttttcttgttcagatcaactttgtatattgtaaag 1575
                                                                                                                                   gcatgttctttgggttgaaaagctgggttatttgatatcttaagattgatgttgttgatc 1635
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                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 193;
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; TOPOLOGY: linear
; MOLECULE TYPE: Oll
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-628-417-6
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                                                                                                                                                                                                       Sequence 3, Patent No.
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Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                           GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #10, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1461 gcattttgatttatgaaaattgttgttgttctttgtatttgtaagatttagtggctagta 1520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                        TITLE OF INVENTION: Procedures and Materials for TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                        119
                                                                                                                                                                                                                                                                                                                                                                                                                          1521 ctttgaatacactgttttgcttttcttgttcagatcaactttgtatattgtaaaggcatg 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                    59
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               118;
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Pred. No. 0.004;
0; Mismatches 117;
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RESULT 13
US-08-587-680A-3
; Sequence 3, Application US/08587680A
; Patent No. 5977434
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REFERENCE/OCCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3921 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 120; Conserv
GENERAL INFORMATION:
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APPLICATION NUMBER: 07-JUN-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product- "Xa-21"
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milarity 49.48;
Conservative
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Pred. No. 0.041;
0; Mismatches 123;
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Ronald, Pamela C.

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; LOCATION: Join(1..2676, 3520..3918)
; OTHER INFORMATION: /product= "xa-21"
US-08-587-680A-3
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC pc-pos/MS-Dos
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LENGTH: 3921 base pair
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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APPLICATION NUMBER: US 00
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
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CURRENT APPLICATION DATA:
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MOLECULE TYPE:
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FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                 TCCAATCTTTCCACTTCGCTTAGTTTTCTTGCACTTGAATTGAATAAGATCACAGGAAGC 1173
                                                                                                                                                     tttttaacaagtttcttattttcttacagggagctttacagtaacaacataactggcccg 2233
ttctccggtcctattccggaatcattgggaaagctttcaaagctgagatttctgtgagta 2353
                                         ATTCCGAAGGATATTGGCAATCTTATTGGCTTACAACATCTCTATCTCTGCAACAACAAT 1233
                                                                         attcctagtaatcttggaaatctgacaaacttagtgagtttggatctttacttaaacagc 2293
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Two Embarcadero Center, Eighth Floor
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Song, Wen-Yuang
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                                                                                                                                                                                                                                                                                        1.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/373,375
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                                                                                                                                                                                                                                                                    Score 46.2; DB 4; Length 3921; Pred. No. 0.041; 0; Mismatches 123; Indels 0
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US-08-475-891A-3
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                                                                                                                         Best Local Similarity Matches 120; Conserv
                                                                                                                                                      Query Match
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TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Procedures unit INTERESTRICTION: Disease Resistance in Plants
TITLE OF SECUENCES: 15
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 06-JUN-19
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MEDIUM TYPE: Floppy disk
                      2174 tttttaacaagtttcttattttcttacagggagctttacagtaacaacataactggcccg 2233
                                                                                       2114 acaaaacaaatccaagatttgacagaagaagcactggagttaccttttgtaattgaaatc 2173
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                                                               1565 AAATTACAAACATTGAACTTGGGAGAAAATAACCTGGGGGGAGTTCTTCCTAATTCGTTT 1624
                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                  OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
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Song, Wen-Yuang
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                                                                                                                          Conservative
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                                                                                                                                                                                                                  join(512..3149, 3993..4393)
RMATION: /product= "RRK-B"
RMATION: /note= "Ra21 Xanthomonas spp. disease
RMATION: resistance gene RRK-B from rice (Oryza
RMATION: sativa)"
                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                            DNA (genomic)
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                                                                                                                                         1.18;
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                                                                                                                                         Score 46.2; DB 3; Pred. No. 0.051;
                                                                                                                          Mismatches 123;
                                                                                                                                                      Length 5992;
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COMPUTER: IBM PC PU 1000

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

CORRENT APPLICATION DATA:

APPLICATION UNMER: US/08/475,891A

FILING DATE: 05-JUN-1995

CLASSIFICATION UNMER: US 08/373,375

FILING DATE: 17-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bastlan, Kevin L.

REGISTRATION NUMBER: 34,774

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 02370-058910US

TELEPHONE: (415) 576-0200

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARROTERISTICS:

LENGTH: 6.25 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FORCISE TURE: DATE: 
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                                                                         Query Match
Best Local Similarity
Matches 120; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Tuang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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LOCATION: join(1648..4383, 5178..5513)
OTHER INFORMATION: /product= "RRK-F"
OTHER INFORMATION: /note= "%a21 %anthomonas spp. disease
OTHER INFORMATION: resistance gene RRK-F from rice (Oryza
OTHER INFORMATION: sativa)"
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STATE: California
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                                                                                           2902 TTCAGAGGGTCACTTCCATCATCGTTGGGCAGGCTTAGAAACTTAGGCATTCTAGTCGCC 2961
                                                                                                                      2294 ttctccggtcctattccggaatcattgggaaagctttcaaagctgagatttctgtgagta 2353
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2962 TAC 2964
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Search completed: June 23, 2000, 22:44:24 Job time: 40210 sec

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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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           BAC End Sequences at ATGC Unpublished (1997) Other_GSSs: T2E10-Sp6
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Feng, J., Dewar, K., B
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A1730535 BNLGH1700
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                                 gtgtatccttacatggccaatggaagtgttgcttcgtgtctca 3643
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Class: BAC ends
High quality sequence
High quality sequence
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Fax: 215-898-8780
Email: jecker@atgenome
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University of Pennsylvania
Dept. of Biology, University of Pe
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Similarity 66.6%;
28; Conservative
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="T2E10"
/clone_lib="TAMU"
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/note="Vector: BeloBACII; Site_1: HindIII; Site_2:
HindIII; Produced by Rod Wing"
275 c 238 g 354 t 13 others
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Location/Qualifiers
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                ttacactaatgacacagagaggccaccgtcacaacctccgcttgattggccaacgcgggaa 3802
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Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utter Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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On Dec 15, 1
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For addtional information,
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sheared to 0.4~0.7 Kbp before ligation."
177 c 112 g 220 t
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/strain="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LERJM53"
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 CGGATGGCACCAAAATCGCTGTAAAAAGATTGACTGATTTTGAACGTCCAGGAGGAGATG
                             cagacggaactcttgttgctgtcaagagactgaaggaagagcgaactccaggtggagagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Contact: Xiaoying Lin
The Institute for Genomic Research
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Class: shotgun
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Fax: 301 838 0208
Email: at@tigr.org
For addtional information,
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                                                                                                                                                          /organism="Arabidopsis thaliana"
/strain="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LERJM53"
/clone="LERJM53"
/clone_ilb="LERG"
/note="Organ: Leaf; Vector: pUC19J
sheared to 0.4-0.7 Kbp before liga
1 a 102 c 154 g 173 t 1
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Kbp before ligation."
173 t 1 others
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hes 212;
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              Unpublished (1993)
On Feb 18, 1999 this sequence version replication for the contact: Shoemaker R/Public Soybean EST Proplect
Public Soybean EST project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Lourel: 314 286 1800
Fax: 314 286 1810
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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                                                                                                                                                                                                 1 (bases 1 to 532)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
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AW233982.1 GI:6566309
EST.
                                                                                                                                                                   McCann,R., Waterston,R. and Wilson,R. Public Soybean EST Project
est@watson.wustl.edu
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                                 TGTCAAAGCAGCTAATATATTGTTGGACGAGGAATTTGAAGCAGTTGTTGGAGATTTTGG
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Pred. No. 1.7
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                                                                                                          aatatctctcaaccggaaaatcttcagagaaaaccgacgttttcggatacggaatcatgc
                                                                 actataaagacactcacgtgacaacagcagtccgtggcaccatcggtcacatcgctccag
                                                                                                                                                                       AATACCTACATGAACACTGTAATCCAAAGATTATTCACCGTGATGTTAAAGCAGCTAATG
                                                                                                                                                                                                                                AGCCTGTTTTGAATTGGCCAACTAGGAAGCGTGTGGCGGTGGGTACTGCACGTGGACTTG 129
                                                 ACGTTAAGAAAACCAATGTGACTACTCAAGTTCGTGGTACAATGGGCCCATATAGCTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On May 7, 1998 this sequence version replaced Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujil, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, Martin, G.B., Tanksiey, S.D. and Giovannoni, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU.
Location/Qualifiers
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100 Jordan Hall, Clemson, SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson University Genomics Institute
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Best Local
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                                                                 GGAGCACTTCCAGATGGCACTAAGATTGCTGTAAAACGGTTAACTGATTACGAAAGTCCT
                                                                                          428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Universitaetsstrasse 1,
Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Annen, F., Chang, J.-L., Paterson, A.H. and Stockhaus Characterization of 14 different putative protein clones of the C4 plant Sorghum bicolor Mol. Gen. Genet. 259 (1), 115-122 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Nov 29, 1993 this sequence version replaced Contact: Stockhaus J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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Similarity 55.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stockha@uni-duesseldorf
                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="green"
/note="Organ: leaf; Vector: Lambda ZAP II; Site_1: Eco
/note="Organ: leaf cDNA library from green leaves,
unidirectionally cloned"
a 194 c 293 g 251 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4558"
/clone="SbRLK2"
/clone_lib="Sorghum bicolor cv. TX430 leaf"
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/strain="cv. TX430"
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Medicago truncatula

Medicago; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; endicotyledons; core
euphyllophytes; Spermatophyta; Magnollophyta; endicotyledons; core
euphyllophytes; Spermatophyta; Magnollophyta; endicotyledons; core
euphyllophytes; Spermatophyta; Magnollophyta; Embaceae; Papillonoideae;
                                                                                                          Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401, USA
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Email: mjharrison@noble.org
Developmental stage: phosphate starved; Date: 01/23/00; Submitted to the Database of Expressed Sequence Tags (dbEST) on 01/26/00; http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                 Harrison, M.J., Liu, J., Gonzales, M.B.
ESTs from phosphate starved roots
Unpublished (1999)
On May 1, 1997 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
AW329855
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N201132e rootphos(-)
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/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                             Location/Qualifiers
1. .475
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1 (bases 1 to 656)
Annen, F., Chang, J.-L., Paterson, A.H. and Stockhaus, J.
Characterization of 14 different putative protein kinase clones of the C4 plant Sorghum bicolor Mol. Gen. Genet. 259 (1), 115-122 (1998)
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EST.
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SDRLK5 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cDNA
SDRLK5 similar to protein kinase, highest similarity to
receptor-like protein kinases, mRNA sequence.
                           Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
                                                                                        Heinrich-Heine-Universitaet
Universitaetsstrasse 1, 402
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/tlssue_type="roots"
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stockha@uni-duesseldorf.de
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Pred. No. 6.7e-25;
0; Mismatches 88;
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Annen, F., Chang, J.-L., Paterson, A.H. and Stockhaus, J.
Characterization of 14 different putative protein kinase cDNA
clones of the C4 plant Sorghum bicolor
clones of the C4 plant Sorghum bicolor
Mol. Gen. Genet. 259 (1), 115-122 (1998)
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Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
                                                                                                                                                    Contact: Stockhaus J
Institut fuer Entwicklungsbiologie und
                                                                                                                                                                          On Jan 13, 1998 this sequence version replaced gi:3421471
Contact: Stockhaus J
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                                               stockha@uni-duesseldorf.
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/clone="SbRLK5"
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ngth: 600 Std Err
Location/Qualifiers
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                                                                                                                                      tggcaaagctaatggactataaagacactcacgtgacaacagcagtccgtggcaccatcg
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GTTACGGCATAATGCTTCTCGA
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/dev_stage="green"
/note="Organ: leaf; Vector: Lambda ZAP II; Site_1:
Site_2: Xho I; leaf cDNA library from green leaves,
unidirectionally cloned"
a 124 c 179 g 183 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sorghum bicolor"
/strain="cv. TX430"
/db_xref="taxon:4558"
/clone="SbRLK4"
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56.1%;
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Pred. No. 1.1e-24;
0; Mismatches 213;
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Best Local Similarity
Matches 207; Conserv
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                                                                                                                                                                        4044 aaaaccgacgttttcggatacggaatcatgcttctaga 4081
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                                  survey sequence.
B27171
B27171.1 GI:2513137
GSS.
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EST.
Oryza sativa.
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p25047
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Fax: 0298-38-7468

Email: minobe@rtcs0.riken.go.

PROJECT ='RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1995)
Contact: Yuzo Minobe
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 299)
Minobe, Y. and Sasaki, T.
Rice cDNA from root
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RICR2976A Rice
                                                                                 B27171 464 bp I
T2E10TF TAMU Arabidopsis
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thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
/strain="%liponbare, sub_species Japonica"
/db_xref="ftaxon: 4530"
/clone="R2976_lA"
/clone="ftay"
/clone="lib="%rice root"
/note="Prepared from seedling root. "
54 c 67 g 85 t
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0; Mismatches 71
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Streptophyta;
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cDNA clone
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 Embryophyta;
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R2976_1A, mRNA
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 Tracheophyta;
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3002 aatttgatttcaggtgggtatggtataactggagcaatagctggtggagttgctgcaggt 3061
                  agcgaactccaggtgg 3497
                                                                                                                                                                                                     CAGCCGAAGAGGACCCTGAGGTTCACTTGGGGCAGCTTAAGCGGTTCTCTCTACGGGAAC
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                                                                                 TTCAAGTAGCAACTGATAGCTTCAGCAACAAGAACATTTTGGGCCGAGGTGGGTTCGGAA
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                                                               AAGTCTACAAATGCCGTCTTGCTGATGGAACACTTGTTGCAGTCAAACGGCTTAAAGAAG
                                                                                                                                                                                                                                                                        GTATTTAGTACTTAATTTTTCAGTTCTGTG----
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis Genomic Unpublished (1997) Other_GSSs: T2E10TR
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Location/Qualifiers
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eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter, J.C.
Use of a BAC End Sequence
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Similarity 64.58;
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/sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1:
HindII; Produced by Rod Wing"
a 87 c 115 g 143 t
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="T2E10"
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Kelley,J.M., Field,C.E., Craven,M.B.,
464
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                                                                                                                                                                                                                               atgatcactgcgatccgaagatcattcaccgtgacgtaaaagcagcaaacatcctcttag
acgaagaattcgaagcggttgttggagatttcgggttggcaaagctaatggactataaag 3963
                                                                                     acactcacgtgacaacagcagtccgtggcaccatcggtcacatcgctccagaatatctct 4023
                                                                   AGACATCTGTGGCTGCTCAGGTCCGTGGAACTATGGGTCACATTGCCCCCTGAATATTTGT
                                                                                                                                         ATGAAGGTTTTGAACCGGTTGTTGGTGATTTCGGCTTGGCCAAGCTGGTGGATGTACAGA 979
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Annen, F., Chang, J.-L., Paterson, A.H. and Stockhaus, J. Characterization of 14 different putative protein kinclones of the C4 plant Sorghum bicolor Mol. Gen. Genet. 259 (1), 115-122 (1998)
98409267
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Universitaetsstrasse 1, 40225 Duesseldorf,
Tel: (49)-211-81-14953
Fax: (49)-211-81-14871
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Institut fuer Entwicklungsbiologie und
Pflanzen
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AA738545.1 GI:3421470
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Sorghum bicolor"
/strain="cv. TX430"
/db_xref="taxon:4558"
/clone="SbRLK3"
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/dev_stage="green"
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Pred. No. 5.3e-23
0; Mismatches 8
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515
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                                      caaccggaaaatcttcagagaaaaaccgacgttttcggat 4062
                                                                                                                                                               acactcacgtgacaacagcagtccgtggcaccatcggtcacatcgctcccagaatatctct 4023
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CAACGGGTCAATCGTCTGAAAAGACTGATGTGTTTGGTT
                                                                                                                           ATTCTCATGTAACGACTGCTGAGGGGCACAGTTGGTCACATTGCTCCAAAATATCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cLEC14J5, mRNA sequence.
AI896277
AI896277.1 GI:5602179
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EST265720 tomato callus,
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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Generation of ESTs from tomato callus tissue
Unpublished (1999)
On May 18, 1998 this sequence version replaced
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Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: David Frisch
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/note="Vector: pBlueScript Sk(-); Site_1: EcoR1; Site
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/clone="clEC14J5"
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AI727837
AI727837.1 GI:5046689
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
AI729440 703 bp mRNA EST 11-JUN-1999
BNLGH113383 Six-day Cotton fiber Gossypium hirsutum cDNA 5' si
to (U93048) somatic embryogenesis receptor-like kinase [Daucus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
ESTs from developing cotton fiber
Unpublished (1999)
On Jun 5, 198 this sequence version replaced gi:3187180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eudicots; Rosidae; eurosids
1 (bases 1 to 597)
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Seq primer: T3 Primer.
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Fax: 516-344-3407
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Similarity 67.8%;
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/lab_host="XL1-Blue"
/note="Vector: pBluescript II KS+"
107 c 165 g 148 t 12 c
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/db_xxe1f-"taxon:3635"
/clone_11b-"Six-day Cotton fiber"
/tissue_type-"immature fiber"
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Pred. No. 2.5e-20;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core

euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core

euticots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

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                                                                                                                                                                     CCACTGGGAAGTCATCAGAAAGAACGGATGTCTTTGGTTATGGGATTATGCTTCTAGA
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A1729440
A1729440.1 GI:5048292
EST
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Seq primer: T3 Primer.
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nilarity 67.8%;
Conservative
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/lab_host="XII-Blue"
/note="Yector: pBluescript II KS+"
/148 c 180 g 186 t 1
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/cultivar-"Acala Maxxa"
/db_xref-"taxon:335"
/clone_lib-"Six-day Cotton fiber"
/tissue_type-"immature fiber"
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Maximum DB seq length: 1000000
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18: em_pl
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(without alignments)
-86.322 Million cell updates/sec
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Compugen Ltd
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45: gb_htg7:*
46: em_htg1:*
47: em_htg3:*
48: em_htg3:*
49: em_hum5:*
50: gb_p13:*
51: gb_pr5:*
52: gb_htg9:*
54: gb_htg1:*
56: gb_htg11:*
57: gb_htg12:*
58: gb_htg13:*
58: gb_htg14:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. a a O 912296 11026 10026 100.0 1106 83.5 1063 82.5 1063 64.6 789 64.6 789 64.6 1789 64.6 1750 7.6 11815 7.6 11815 7.0 84440 7.0 118086 6.7 101284 6.5 100887 6.4 112529 6.3 134402 6.1 181402 6.1 181402 6.1 181402 6.1 181402 6.1 181402 6.1 181402 6.1 181402 6.2 100887 6.4 112529 6.3 114402 6.3 115944 6.1 88401 6.1 88401 6.2 100887 6.4 112529 6.3 134402 6. Query Match Length 멂 ATAC009991 A67815 AC012654 O ATAC011620 E12705 ATU47029 AC021198 AB010075 ATF6H11 INU77888 AP000815 A67796 SBU62279 LELRPGENE DCU93048 A67797 AC015446 ATAC011765 AC008017 AB029327 F23M19 AB012239 ATF17M5 ATF1C12 A67817 A67819 A67825 A67821 A67823 A67823 AC005957 AB017061 AC003981 AC003981 A57133 U42445 A57130 AB011476 AB028616 SBRLK1 AB010698 X95269 L.esculentu U93048 Daucus caro A67797 Sequence 2 AC021198 Arabidops AB010075 Arabidops AB010075 Arabidops AB010075 Arabidops AB0100815 Oryza sat A67796 Sequence 1 AC009991 Arabidops AC011620 Arabidops E12705 Arabidopsis AC011544 Arabidops E12705 Arabidopsis AC011765 Arabidops E12705 Arabidops AC011765 Arabidops AC01765 Arabidops A67817 Sequence 22 A67819 Sequence 24 A67825 Sequence 26 A67821 Sequence 26 A67821 Sequence 28 A67823 Sequence 32 U62279 Sorghum bic X95269 L.esculentu Description

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De.V.S., Schmidt,E.D., Van,H.G. a
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                                                             TGCGCCTGAGCTTGGGAAGCTTGAACATTTACAGTATCTAGAGCTCTACAAAAACAACAT
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De,V.S., Schnidt,E.D., Van,H.G. a
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unidentified"
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/note="unnamed protein pi
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Pred. No. 1.4e-208;
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Sequence :
A67821
A67821.1
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De, V.S., Schmidt, E.D., Van, H.G. a
PRODUCTION OF APOMICTIC SEED
PRIENT: WO 9743427-A 20-NOV-1997;
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                                                                                                               'note="unnamed protein product"
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RESULT 5
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Sequence
A67823
A67823.1
1 (bases 1 to 894)
De, V.S., Schmidt, E.D., V
PRODUCTION OF APOMICTIC
                                    unidentified unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctccgaaggagatgctctctacgctcttcgccggagttttgacagatccagaccatgtcct
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ESYSELYKNEIQGTIPSELGNLKSLISLDLYNNNLTGKIPSSLGKLKSLVFLRLNENR
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Pred. No. 4.5e-69;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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/db_xref="GI:475650".1"
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NVLQSWDPTLYNPCTWFHYTCNNENSVIRYDLGNAELSGHLYPELGVLKNLQYLELYS
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Isolation of a cDNA encoding a novel leucine-rich repeat motif
Sorghum bicolor inoculated with fungi
Mol. Plant Microbe Interact. 9 (9), 819-825 (1996)
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                                                                       Conservative
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                                                                                                                                                                                 /PIOTEIN_Id="AAC49559.1"
//DIXEGE="GL:1710124"
//db_xref="GL:1710124"
//db_xref="GL:1710124"
//db_xref="GL:1710124"
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NGSIPETLGNLTNLISLDLAWDNLLTGELFTTLGSVSTLRYLRLYQNNLTGPIPSSFGN
LTSLLESKLODNSLGGALPASLGNIKALOFSRLNDNMLTGTVPSKSFPLSTFGNLTEL
NTDRNNLDGTRTSSGLRVTAIIQDALKTA"
36. .77
/evidence=not_experimental
/evidence=not_experimental
232 c 207 g 250 t
                                                                                                                                                                                                                                                                                                                                                                                                      /function="protein-protein ligand binding"
/note="leucine-rich repeat-containing extracellular
glycoprotein; contains six N-glycosylation sites
[NX(S/T)]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Sorghum bicolor"/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'clone="SLRR"
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                                                                   Score 151.2; DB 8 Pred. No. 3.1e-26; 0; Mismatches 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-JAN-1996) P. Vera, Universidad Politecnica de Valencia, Inst. de Biologia Molecular y Celular de Plantas, de Vera 14, E- 46022 Valencia, SPAIN

2 (bases 1 to 4604)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
esteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
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X95269
                                                                                                                                                                                                                                                                                                                                                                                           Tornero,P., Mayda,E., Gomez,M.D., Canas,L., Conejero,V. and Vera,P. Characterization of LRP, a leucine-rich repeat (LRR) protein from tomato plants that is processed during pathogenesis Plant J. 10 (2), 315-330 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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/gene="LRP"
              /Codon_start=1
/product="LRR protein"
/protein_1d="CaA64565.1"
/protein_1d="CaA64565.1"
/db_xref="GI:1619300"
/db_xref="GFTREMEL:096477"
/db_xref="SPTREMEL:096477"
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SDEGNYLOSNPPNLYNFCTNFEHVTCNCDNOVTRVDLGNSKLSGHLVPELGKLEHLQYL
ELYKNNIQGTIPKELGNLKSLISLDLYNNNISGTIPTSLGNLKNLVFLRLNDNKLTGP
                                                                                                                                                                      join(113. .345,2381.
4283. .4355)
                                                                                                                                                                                                                                                                                                            /organism="Lycopersicon
/cultivar="VFN8"
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<1. .345
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LPRELTSISSLKVVDVSNNDLCGTIPTSGPFEHIPLNNFEHNPRLEGPELLGLATYDJ
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Best Local Similarity 69.1%;
Matches 132; Conservative
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Daucus carota

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

1 (bases 1 to 1755)
Schmidt, E. D., Guzzo, F., Toonen, M.A. and de Vries, S.C.

A leucine-rich repeat containing receptor-like kinase marks somatic
plant cells competent to form embryos
Development 124 (10), 2049-2062 (1997)
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U93048.1 GI:2224910
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3153. .428
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Pred. No. 3.7e-13;
0; Mismatches 59;
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2 (bases 1 to 1755)
2 (bases 1 to 1755)
Schmidt, E.D.L., Guzzo, F., Toonen, M.A.J. and de ....
Direct Submission
Submitted (12-MAR-1997) Molecular Biology, Agricultural University of Wageningen, Dreyenlaan 3, Wageningen 6703 HA, The Netherlands Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  CTTGCGTCTCAACAACAACAGCCTCTCTGGTCCAATTCCAATGTCACTGACTAATATTAC
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Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                             A67797 1815 bp DNA
Sequence 2 from Patent WO9743427
A67797
                                           carrot.
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VRGTLCYIAPEYLISTGKSSEKTDVFGYGIMLLELITGGRAFDLARLANDDDVMLLDWV
KSLLKEKKLEMLVDFDLENNYLDTEVEQLIQVALLCTQGSPMERPKMSEVVRMLEGDG
LAEKWDEWQKVEVIHQDVELAPHRISEWILDSTDNLHAFELSGPR*

3 47 c 407 g 495 t
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Pred. No. 3.5e-10;
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De, V.S., Schmidt, E.D., Van, H.G. and Hecht, V.F.
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
                                         sequence.
AC021198
AC021198.2
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Arabidopsis thaliana chromosome
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MILTNLYSLDLYMMSFSGPIPDTLGKLTRLRFLKNINISLSGPIPMSLTMITTLQVIDL
SNRTLSGPYDDMOSFSLETPISFANILMLGGYTGRCOGESPEFSPTBPIPSTVOD
PGONGPTGAIAGGVAAGAALLFAAPAMAFAWWRRKPREHFFDVPAEEDPEVHLGQLK
RFSLRELQVATDTFSTILGRGGFGKVYKGRLADGSLVAVKRLKERTPGGELDFQTKTV
EMISMAVHRULLELRGCOMTPTERLLTVYPYMAGSVASGLTEROPSEDPLDWFTRKT
ALGSARGLSYLHDHCDFKIIHRDVKAANILLLDEEFEAVVGDFGLARLMDYKDTHVTTA
VRGTLGYIAPEKLSTGKSSEKTDVFGYGOMLLELITGGRAFDLARLANDDVKMLDWV
KSLLKEKKLEMLVDPDLENNYIDTEVEQLIQVALLCTGGSPMERFKMSEVVRMLEGDG
LAEKWDEMOKVEVIHQDVELAPHRTSEWILDSTDNLHAFELSGPR"

354 c 415 g 515 t
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/db_xref="taxon:4039"
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/db_xref="GI:4756624"
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                 2766 TCATTCC
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plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA On Feb 11, 2000 this sequence version replaced g1:6693723. The sequence is of BAC F14D7 from Arabidopsis thaliana chromosome 1. The sequence does not represent the sequence of the entire insert of this clone. It is shorter by 6954 bp because we submit only the unique sequence of the clone. However, in order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide small overlaps (200 bp) between overlapping sumbitted clones. The 5' end of this sequence overlaps by 200 bp to the 3' end of the sequence of the clone
                                                                                                                                                                                                                                                                                                               CTATTCTTTATCTTTACGAGAACTATTTAACTGGTGTCATTCCCCCGGAACTAGGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                        TGAGTAACAACAAACTTACCGGTTCAATTCCTTCCTTAGGAAATCTCAAGAATTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTAACTGGTGGCATTCCCCCGAAACTAGGCAACATAGAATCCATGATCGATTTAGAGT 2525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatctagagc 442
                                                                                                                                               tcagcttggatctgtacaacaacatcttacagggatagttcccactttcttgggaaaat 562
                                                 caatccc
                                                                                                                                                                                                                                                        tgaagtetetggtetttttaeggettaatgacaacegattgaeeggteeaateetagage 622
                                                                                                   CCTTCGGAAATCTCAAGAACTTGACGTATCTTTATCTTTACCTGAATTATTTAACTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-JAN-2000) P. Street, Albany, CA 94710, 3 (bases 1 to 81513)
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
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Pred. No. 3.9e-09;
0; Mismatches 142;
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                                                                                                                                                                                                                                                                                                      gaagtetetggtetttttaeggettaatgaceaecegattgaeeggteeaateetagagea 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCTAACAACATGTTCACCGGAGAGATTCCAGCGAGTTTCGCAGAGTTGAAGAATCTCAC 35148
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  ATF6H11 118086 bp
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Structural Analysis of Arabidopsis thaliana Chromosome Unpublished (1998)
(bases_1 to 84440)
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Arabidopsis thaliana
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Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan
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/chromosome="5"
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EU Arabidopsis sequencing, project.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidoṛsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
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Bevan, M., Brandt, P., D
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E-mail: michael.bevan@bbsrc.ac.
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KAKKAKVHALSELKQVVMAHALAKKTVVDEGGVFVISSLLSPFTSHAVGSBAIALIV

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VVTDEKKKLDLKEMISELELPEIPSVFTCPISLEPMQDPVTLCTGQTYERSNILKWFN
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/gene="F6H11.10"
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VKFTPRNGTGVLVICPTRELAIOSYGVAKELKKYHGQTVKVIGGEKKIETEAEILAKG
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GGILLCTINVAARGLDFPHVDWTYGVDFPDNFTDYIHRYGTTAGGGAKGKALLVLTP
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BLKFTGYLKAAKIPVEBHEFEBKKLLDYKFFVENLISENYALKESAKBAYKTYISGYD
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4961. .52
                               complement(7445.
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/product="DEAD box ATP dependent helicase protein"
/protein_id="CAA16673.1"
/db_xref="GI:2827700"
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/gene="F6H11.10"
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              /number=6
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             GCCGGAGCTTGAAGTGTTACAGCTTTGGGAGAACAATTTCACCGGAAGCATCCCGCAGAA 84539
                                                                                                cagcitggalctgtacaacaatcttacagggalagttcccactttcttgggalaatt 563
                                                                                                                                                        GTCTAACAACATGTTCACCGGAGAGATTCCAGCGAGTTTCGCAGAGTTGAAGAATCTCAC 84659
                                                                                                                                                                                                                             CTTCTCCGGTCCATTAACTTGGGAGCTAGGAACGCTATCGAGTTTAAAAATCAATGGATTT 84719
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Similarity 52.3%;
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KLLLPKKSLKRAQIHRQPKHYLNSQALCSSRTGGITKEMGSHLKREVQQRHYSTEHT
AFETTGINRGCLLSEISAVLSDIGGLYTTAAVMTHHERAAWIYLEDGFMGGPITDFI
RKAQVKDHLDTVMEAHHIVGDVSHVVVRVVEAKGVPVGWAHTERRLHELMYGEGDYEN
CFDCDCFGDRCDALWRGRCERIHVTIEACNGYSMVNVCCNDREVLLFDTVCALKELQF
VYFHAVAGAKGSTAEDEFIIRKNGCTLETEGORERLHFLIVAAISRASAGGIKLEIR
TENKMGLLSDVTRVVRENGLSITRAEMCTQGEIAVGSFYVTDVNGGETGPSEVEAVVR
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/note-"similarity to predicted protein, Arabidopsis thaliana, C80DDT21F"
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9707. .14616
/gene="F6H11.30"
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/number=3
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/protein_id="CAA16674.1"
/db_xref="G1:2827701"
/db_xref="SPTREMBL:049531"
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Bassett,C.L., Cohen,R.A., Nickerson,M.L. and Rajeevan,M.S.
Direct Submission
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Convolvulaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Station,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bassett,C.L., Cohen.R.A., Nickerson,M.L. and Rajeevan,M.S. Identification and Preliminary Characterization of an Unusual Leucine-rich Repeat Receptor-like Protein Kinase from Morning Glory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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45 Wiltshire Road, Kearneysville, WV 25430, USA
Location/Qualifiers
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/tissue_type="young leaf"
237. .251
                                                   SMVREIETIGKVRHRNLIKLEEFWLRKEYGLILYTYMENGSLHDILHETNPPKPLDNS
TRHNIAVGTAHGLAYLHFDCDPAIVHRDIKPMNILLDSDLEPHISDFGIAKLLDQSAT
SIPSNTVQGTIGYMAPENAFTTVKSRESDVYSYGVVLLELITRKKALDPSFNGETDIV
                                                                                                                                                                                                                                                                                                                                                                           /gene="inrpk1"
join(1144. .4108,4202. .4566)
/gene="inrpk1"
                         GWYRSYWTQTGEIQKIYDPSLLDELIDSSYMEQYTEALSLALRCAEKEYDKRPTMRDV
YKQLTRWSIRSYSSSYRNKSK"
                                                                                                                                                                                                                                                                                                            /product="receptor-like protein kinase"
/protein_id="AAB36558.1"
/db_xref="GI:1684913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Ipomoea nil"
/cultivar="Violet"
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Query Match
Best Local s
Matches 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1341 GAGACAATTTGTTGATACTCTGAACCTCTCCTCCTATGGAATCTCAGGCGAATTCGGGCC 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1281 CCAGAGCTGGAATGCTTCAGATTCCACTCCTTGTTCATGGCTGGGAGTAGAATGTGACAG 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1461 CTCAATTCCTTCCCAGCTAGGCAATTGCAGTCTTCTTGAACACATAGATCTGTCCTCCAA 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1401 CGAAATCTCGCATTTGAAGCATTTGAAGAAGGTTGTTCTCAGTGGCAATGGTTTCTTTGG 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 agacaaccgcgtcactcgtgtggatttgggaaattcaaacctctctggacatcttgcgcc 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 ccagagctgggatccaactcttgttaatccttgtacctggttccatgtcacctgtaacca 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  645 taaagttgttgacgtctcaagcaatgatttgtgtgggacaatcccaacaaa 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 6.9%; Local Similarity 49.1%; nes 202; Conservative
                                                                                    Direct Submission

AL Submitted (30-NoV-1999) to the DDBJ/EMBL/GenBank databases. Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program, Kannondal 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp,
URL:http://www.dna.affrc.go.jp.
URL:http://www.dna.affrc.go.jp.82/, Tel:81-298-38-7441,
Fax:81-298-38-7468)
The orientation of the sequence is from T7 to SP6 of the PAC clone. Genes were predicted from the integrated results of the following:GENSCAN1.0, BLASTN2.0, BLASTN2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against the non-redundant database NRP (PIR, SWISSPROT, GENPEPT, PDB) from MAFF DNA bank and the cDNA sequence database at RGP. Protein similarities of the cording regions were searched against NRP with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone TD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgagcttgggaagcttgaacatttacagtatctagagctctacaaaaacaacatccaagg 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGTTCTTTAATTCTCTGATTGGCCCATTTCCTGAGTCTTTACTTTCAATTCCACATTT 1640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 142418)
Sasakl.T., Matsumoto,T. and Yamamoto,K.
Oryza sattya nipponbare(GA3) genomic DNA,
clone:P0003H10
Detailed information on assemble quality together with annotation of this entry at http://www.dna.affrc.go.jp:82/genomicdata/Genomeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki, T., Matsumoto, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Only in DataBase (1999) In press 2 (bases 1 to 142418)
                                                                         no. and RGP clone ID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poaceae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sativa (cultivar:Nipponbare) DNA, clone:P0003H10
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Pred. No. 2.3e-08;
0; Mismatches 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Yamamoto, K.
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FEATURES
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//note-"ESTS D47452(S12946),C23573(S10086),C19173(E10057),  
AU081294(E10057),AU032455(S10086) correspond to a region  
AU081294(E10057),Similar to PNIL34. (U37437)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="ESTs AU081256(C53656), AU081257(C53656), AU03236(R3784), AU081351(E61905), AU031587(E61905), AU031361(R3784) correspond to a region of the predicted gene.; Similar to alien-like protein. (AC005623)"/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_1d-"BAA87823.1"
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/db_xref-"G1:6498420"
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PAAKPGTPKRKGKTETGETLLTPRFYTTDEDEMERLFNAEINKOLNQEEEFDALLQEFK
TDYNQTHFVRNPEFKAAADKMEGPLRQIFVEFLERSCTAEFSGFLLYKELGRRLKKTN
PVVAEIFSLMSRDEARHAGFLNKGLSDENLALDLGFLTKARKYTFFKPKFIFYATYLS
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RYDKKENPYNRGAISNIAEVFCAGIPPSMNNFRSWVAPPPLEEPDDVSGQLPPRNGAD
LTGGVKEKVDLEMGRNGGIIPAILRGLDYDEMEKNDVSVHIKDRGAAPAAPDPFWAGR
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PESCGGGDEBECVAGDVTFSREWYTAASPHLRLFRSKDVVVNGCVVKVKYCDTCLLXF
PPRASHCSICNNCVRKFDHHCPWVGQCIGLRNYRFFFLFISTSTLLCVYVFVVSMLNI
                                                                                                                                                                              join(22475. .22550,23332. .23705)
/note="ESTs AU030013(E50493), correspond
/note ESTs AU030013(E50493), correspond
to a region of the predicted gene; Similar to O.sativa
gene encoding calmodulin. (Z12828)"
                                                                                                                                                                                                                                                                                                                                                                 NY IEDLLKNIRTQVLLKLIKPYTRIRIPFISQKWCMKIISNMELWY ILVLFHGTLYYT
RAILGSCKKYSLKLDLFLSCAQTRYQLKSCALNRADPMLFLTEVNLLSYSYQDALSSI
VLSMFCMELNFPEKDVEQLLYSLILDNRIQGHIDQVNKLLERGDREIFPSHRQVEYSAE
EHLPNGVQQSMYREIAGCLGCTALGTCLHVLLMWMLGFCPELMLSANSNESETILASM
ARNFWFCWHCRTSKFWYGRENVWFRVKYAPGTRHTANIVPLPSSDSVANQSLSNQNEG
KESPFLSYTTDQQALNLQREHTTLSDNVINLSEGSYRPLAPSSHLGHPYYTIFYVDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILKELHKSCQREDGSDDQKKGTQLLEVYAIEIQMYTETKNNKKLKELYTKALSIKSAI
PHPRIMGIIRECGGKMHMAERQWADAATDFFEAFKNYDEAGNPRRIQCLKYLVLANML
MESEVNPFDGQEAKPYKNDPEILAMTNLIAAYQKNDIMEFEKILKSNRRTIMDDPFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_1d="BAA87824.1"
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IMDFYSGSASQNFSLLQEFYQTTLKALEEAKNERLMFKTNLKLCKIWFDNGEYGRMSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(13373 . 13457,15836 . 15914,17237 . 17477,17560 . 1)
17726 . 17860,18400 . 18587,18681 . 18749,18826 . 18916,
19028 . 19162,19323 . 19379,19349 . 19441,19450 . 19509,
19523 . 19585,19589 . 19701,19800 . 19941,20057 . 20294,
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KAKLWSRFFCLSVYVIMYLNDCQRTTFYEGIGLDTKEFDMHVIIETNRTTARIFPAVL
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BAC clone F22K18 (AL035356)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4530"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESGSVDFAEFEPQLVY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(2901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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TeaelQdmineydadgngtidffeeflnlmarkmkdtdseeelkeafryfdkdQngfis
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                                                                                                                                               codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21586)
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GGGVVVAHKRRSGAREEERRCGGFERRSGGDERGGVREEEDKAEPVGRRENKGERIGE
TDERRKPGHSHKPILLMWIQTTKPARRFGANVLARHGGDDRRRCRSGCAVARRRQE
ALPIGSLFPLLYFMIBUKVAKEEGDUGFYAGFVASGCIVQAVASEVCRKEHQALGISL
VTSSRAIALVVGPAIGGFLSQETLHMHHDDKEVIDALEAQDATSDLGETTKESGSGRM
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complement(join(24778. 24897,25615. 25722,25808. .25893,

26090. .26177,26435. .26538,27519. .27581,27708. .27778,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MERGRGRAPATACGSVRCYAAEVAPEQEDSARYALLLLIRLRDSP
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translation~"MAAAWSPALAAVLLAAAVASASNSEGDALYALRRALADPRGVLQ/

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Search completed: June 24, 2000, 00:15:32 Job time: 45887 sec
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                                                                                                                                                                                                                53685 CTTGGCAAGCTGAGTTCCTTAGTATTCTTGTGAGTAACT 53647
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                                                                                                                                                553 ttgggaaaattgaagtctctggtctttttacggcttaat 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWDPTLVNPCTWFHVTCDRAGRYTRLDLGNSNLSGHLAPELGHLEHLQYLELYKNNIQ GTIPAELGSLKNLISLDLYNNNITGTIPKELGKLSSLVFLRLNDNSLNGFIPROLAKI SSLKVLDVSNNNLCGTIPTSGPFEHIPLNNFDKNPRLEGPELQGLATYDTNC" 59608. .59826 /_ncte="hypothetical protein"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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CF-5 pathogen resi
O. longistaminata
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Pear polygalacturo
Arabidopsis steroi
Maize Xa21 gene DT
Arabidopsis thalia
Tomato Xa21 clone
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Maize Ka21 gene DT
Rice Ka21 disease
O. longistaminta X
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D 20-NOV-1997.

E 13-MAY-1997; EG:2443.

R 14-MAY-1996; GE-010044.

A (NOVS) NOVARTIS AG.

A (NOVS) NOVARTIS AG.

I De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

R WPI; 98-086529/08.

R P-PSDB; W47018.

T Production of apomictic seeds - useful in plant breeding

C Claim 28; Pages 71-73; 123pp; English.

T Production of apomictic seeds - useful in plant breeding

C Claim 28; Pages 71-73; 123pp; English.

C SERK LERR (leucine-rich repeat) sequences.

C Sequence 1106 BP; 331 A; 258 C; 206 G; 311 T;
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Best Local Similarity
Matches 1106; Conserv
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03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST receptor kinase; apomixis; apomictic; seeds; plant breeding; leucine-rich repeat; ss. plant breeding; leucine-rich repeat;
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v06587;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST cl
receptor kinase; apomixis; apomictic; seeds; pr
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Location/Qualifiers
CDS
104..760
WO9743427-A1.
20-NOV-1997.
13-MAY-1996; GB-010044.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, $
WPI; 98-086529/08.
P-PSDB; W47019.
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                                                                                                Location/Qualifiers
104..760
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/note- "shows high hc
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production;
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Best Loc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match
L Local Similarity
ches 952; Conserv
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                                                                                                                                     ttgcaagctacgacactaactgcacctgaaacaactggcaaaacctgaaaatgaagaatt
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                                                                                                                                                                                                                                                                                                                                                                                                accttccgaacttggaaatctgaagaatctcatcagcttggatctgtacaacaacaatct
                                                                                    ggggggtgaccttgtaagaacacttcaccactttatcaaatatcacatctattatgtaat
                                                                                                                                                                                                                                                                                                                                                                                     ACCTTCCGAACTTGGAAATCTGAAGAATCTCATCAGCTTGGATCTGTACAACAACAATCT
  totcaattgagaacttcgaggtctgtatgtaaaatttctaaaatgcgattttcgcttactg
                                                    aagtatatatatgtagtaaaaacaaaaaaaatgaagaatcgaatcggtaatatcctctgg
                                       AAGTATATATGTAGTAAAAACAAAAAAAATGAAGAATCGAATCGGTAATATCATCTGG
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nilarity 98.8%;
Conservative
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Pred. No. 1.3e-225;
0; Mismatches 10;
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20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
14-WAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-086599/08.
P-PSDB; W47022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST receptor kinase; apomixis; apomictic; seeds; plant breeding; leucine-rich repeat; ss. Arabidopsis thaliana.

Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Production of apomictic seeds - useful in plant br Claim 28; Pages 86-88; 123pp; English.
The sequence is that of an EST clone showing high SERK LRR (leucine-rich repeat) sequences.
Sequence 1063 BP; 313 A; 242 C; 206 G;
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                         tgcgcctgagcttgggaagcttgaacatttacagtatctagagctctacaaaaacaacat
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caacaaccaatcttacagggatagttcccactttcttgggaaaattgaagtctctggtctt
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                                                                                                      TAACCAAGACAACCGCGTCACTCGTGTGGATTTGGGGGAATTCAAACCTCTCTGGACATCT
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95.0%;
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Pred. No. 1.2e-222;
0; Mismatches 36;
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Best Local Similarity 96.
Matches 753; Conservative
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21-NOY-1997; E02443.
13-MAY-1996; GB-010044.
(NOYS) NOVARTIS AG.
De Vries SC, Hecht VFG, SWPI; 98-086529/08.
                                                                                                                                                                                                   03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous receptor kinase; apomixis; apomictic; see plant breeding; leucine-rich repeat; ss. Arabidopsis thaliana.
Location/Qualifiers CDS 2..664
                                                                                                                                                                                                                                                                V06588;
                                                                 Production of apomictic seeds - useful in pla
Claim 28; Pages 79-80; 123pp; English.
The sequence is that of an EST clone showing
SERK LRR (leucline-rich repeat) sequences.
Sequence 788 BP; 234 A; 191 C; 156
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                        Score 714.2; DB 1;
Pred. No. 2.2e-172;
0; Mismatches 28;
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V06589;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST cl
receptor kinase; apomixis; apomictic; seeds; pr
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Location/Qualifiers
CDS
1..678
WO9743427-A1.
20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
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Best Local Similarity 71.9%;
Matches 532; Conservative
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P-PSDB; W47021.
Production of apomictic seeds - useful in pla Claim 28; Pages 83-84; 123pp; English.
The sequence is that of an EST clone showing SERK LRR (leucine-rich repeat) sequences.
Sequence 894 BP; 270 A; 163 C; 176
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                                cctgaaacaactggcaaaacctgaaaaatgaagaattggggggtgaccttgtaagaacact 853
                                                          acaacccgagattggagggaccggaattactcggtcttgcaagctacgacactaactgca
                                                                           GAGTCTAATCAGTTTGGATCTGTACAACAACAATCTCACCGGGAAAATCCCCATCTTCTTT
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Pred. No. 7.5e
0; Mismatches
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The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant the developed into plant progeny. This is useful in plant can be developed into plant progeny. This is useful in plant the case that sexual plants are available as crosses with the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding programs combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 314
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20-NOV-1997.
13-MAY-1997; E
14-MAY-1996; C
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gcctttaaagttgttgacgtctcaagcaatgatttgtgtgggacaatcccaacaacgga
                                                                                                         aacaacaatcttacagggatagttcccactttcttgggaaaattgaagtctctggtcttt
                                                                                                                                    ACTGGCCCGATTCCTAGTAATCTTGGAAATCTGACAAACTTAGTGAGTTTGGATCTTTAC
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                                   CTCCGGCTTAACAACAACAGTCTCACTGGGTCAATTCCTATGTCACTGACCAATATTACT
                                                          ttacggcttaatgacaaccgattgaccggtccaatcctagagcactcacggcaatcccaa
                                                                                    TTAAACAGCTTCTCCGGTCCTATTCCGGAATCATTGGGAAAGCTTTCAAAGCTGAGATTT
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/product= SERK protein
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Pred. No. 1.9e-39;
0; Mismatches 205
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Best Local Sim
Matches 188;
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of the embryo sac. The apomictic seeds and embryos thus produced
can be developed into plant progeny. This is useful in plant
breeding programs. Controllable and reproducible apomixis provides
many advantages in plant improvement and cultivar development in
the case that sexual plants are available as crosses with the
apomictic plant. Apomixis provides for true-breeding, seed
apomictic plant and could shorten and simplify the breeding
process so that selfing and progeny testing to produce and/or
stabilise a desirable gene combination could be eliminated.
Apomixis allows plant breeders to develop cultivars with
seed and forage quality and maturity.
Seed and forage quality and maturity.

Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;
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The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel containing
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20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
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Similarity 52.1%;
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Daucus carota SERK greceptor kinase; apo
plant breeding; ds.
Daucus carota.
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13-MAY-1997; ED2443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, SWPI; 98-086529/08.
        production of apomictic seeds - useful in plant breeding Claim 21; Pages 40-46; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provide
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6197. .63
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WO9743427-A1.
20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
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Arabidopsis thaliana SERK receptor kinase; apomixis;
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5295. .58
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3731. .3802
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Pred. No. 1.4e
0; Mismatches
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The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac: The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed apomixis allows plant breeders to develop cultivars with seed apomixis allows plant breeders to develop cultivars with seed apomixis allows plant breeders to develop cultivars with seed apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
DNA encoding plant morphogenesis regulatory protein - useful yield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 1/pp; Japanese.
The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to a plant with, e.g. short stems or altered inflorescence. The acts on a plant at a specific site for a specific period, and
                                                                                                                                                                                                                                           04-MAR-1997.
24-AUG-1995; JF-216187.
24-AUG-1995; JF-216187.
(MITS-) MITSUI GYOSAI SHOKUBUTSU
(CHIK-) ZH CHIKYU KANKYO SANGYO (WPI; 97-206629/19.
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WPI; 98-086529/08.
P-PSDB; W47017.
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Arabidopsis thaliana plant morphogenesis regulatory protein cDNA.
Plant; morphogenesis; regulation; short; stem; alteration;
inflorescence; extraneous; gene; expression; transformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUN-1997
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/note- "plant morphogenesis regulatory protein"
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70.3%;
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Best Local
                                                                                                                                                                                                                                                                                                23-NOV-1995.
11-MAY-1995; G01075.
11-MAY-1994; GB-009394.
23-DEC-1994; WO-G02812.
31-MAR-1995; GB-006658.
07-APR-1995; GB-007232.
Increasing plant pathogen resistance by induction of variegation—may lead to acquired resistance to a broad range of pathogens.

Claim 9; Page 85-87; 13pp; Engilish.

T06307 is a tomato pathogen resisitance gene Cf-2.2 partial cDNA clone. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.2 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fullyum. C.fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 3573 BP; 1032 A; 654 C; 664 G; 1223 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therefore be used to regulate extraneous gene expression in plant. The MRP'S CDNA or genomic DNA can be used to transfor plant to increase its MRP expression, and therefore control form (particularly stem length) of the plant.

Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;
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Pred. No. 7.1e-09;
0; Mismatches 147
                                                                                                                                                                                                                                                                  Jones JDG;
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Avr 4; Avr 9;
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Query Match Best Local Similarity

52.2%;

Score Pred.

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Query Match
Best Local Similarity
Matches 142; Conser
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11-MAY-1995; G01075.
11-MAY-1994; GB-009394.
23-DEC-1994; WO-G02812.
31-MAR-1995; GB-006658.
07-APR-1995; GB-007232.
                                                            increasing plant pathogen resistance by induction of variegation may lead to acquired resistance to a broad range of pathogens.

Claim 9; Page 80-83; 111pp; English.

706306 is the tomato pathogen resisitance gene Cf-2.1. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.1 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulvum.

C.fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 6471 BP; 2073 A; 1106 C; 1122 G; 2170 T;
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Pathogen resistant; Cf-2.1;
leaf mould; variegation; ds.
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  Conservative
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5015. .6471
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1677. 1745
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1746. .5011
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1. .1676
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           52.2%;
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Score 64; DB 1;
Pred. No. 4.8e-07;
0; Mismatches 130
                                                                                                                                                                                                                                                                Jones JDG;
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                                                                            PS Claim 3; Fig 1a; 75pp; English.

PS Claim 3; Fig 1a; 75pp; English.

CC This sequence is an example of the polynucleotide of the invention, and CC is able to confer pathogen resistance on a plant. It is one of two tomato CC the gene variants, which offer resistance against the pathogen CC CF-5 gene variants, which offer resistance apainst the pathogen CC cladosporium fulvum-5. Transgenic plants can be produced by incorporating CC the gene into plant cells and regenerating plants from the cells; CC assaually or sexually produced offspring can also be subsequently CC produced. Expression of the gene in plant cells can confer pathogen CC resistance on a plant e.g. to tomato leaf mould (C. fulvum) in tomatoes. CC oligonucleotides with sequences complementary to the gene expression. The nucleic acids/polynucleotides are useful as hybridisation probes to CC identify other genes/fragments conferring pathogen resistance on plants CC e.g. phytophthora resistance in potatoes. Homologies between Cf-5 and CC cf-9 may be used to identify further resistance genes of this class.

SQ Sequence 3979 BP; 1217 A; 717 C; 698 G; 1347 T;
                                                                                                                                                                                                                                                                                                                                                                  Tomato gene Cf-5, confers resistance to Cladosporium fulvum -
for production of transgenic plants resistant to pathogens e.c
tomato leaf mould C. fulvum in tomatoes
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20-NOV-1997.
08-MAY-1997; G01249.
24-SEP-1996; GB-019924.
09-MAY-1996; GB-009681.
(INNE-) INNES CENT INNOVATIONS LTD JOHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF-5 pathogen resistance gene variant #1.
Tomato; CF-5 pathogen resistance gene; Cladosporium fulvum-5;
tomato leaf mould; Phytophthora resistance; ss.
Lycopersicon pimpinellifolium.
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20-MAY-1998
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653. .3560
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Score 61.2; DB 1;
Pred. No. 2.1e-06;
0; Mismatches 173;
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                                                                                                                                                                                                                                                                                                                              Frank; W415U.

For Tomato gene Cf-5, confers resistance to Cladosporium fulvum - useful production of transgenic plants resistant to pathogens e.g.

For tomato leaf mould C. fulvum in tomatoes

PS Claim 6; Fig 1b; 75pp; English.

CT his sequence is an example of the polynucleotide of the invention, and cis able to confer pathogen resistance on a plant. It is one of two tomato CC CF-5 gene variants, which offer resistance against the pathogen cC Cladosporium fulvum-5. Transgenic plants can be produced by incorporating cC cladosporium fulvum-5. Transgenic plants can be produced by incorporating cC caseaually or sexually produced offspring can also be subsequently cC produced. Expression of the gene in plant cells can confer pathogen cC cesistance on a plant e.g. to tomato leaf mould (C. fulvum) in tomatoes.

CC Oligonucleotides with sequences complementary to the gene or fragments confering other gene expression. The cc clearity other genes/fragments conferring pathogen resistance on plants ce.g. Phytophthora resistance in potatoes. Homologies between Cf-5 and CC c.g. Phytophthora resistance in potatoes. Homologies between Cf-5 and CC c.g. against class.

So Sequence 3979 BP; 1218 A; 716 C; 698 G; 1347 T;
                                                                                                                                                                                       Query Match
Best Local S
Matches 165
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20-NOV-1997.
08-MAY-1997; G01249.
24-SEP-1996; GB-019924.
09-MAY-1996; GB-009681.
09-MAY-1996; GB-009681.
(INNE-) INNES CENT INNOVATIONS LTD JOH
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Tomato; CF-5 pathogen resistance gene; Cladosporium tomato leaf mould; Phytophthora resistance; ss.
Lycopersicon pimpinellifolium.
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                                                              2023 TTACTGAACTATTTTTGGGTAATAACTCTCTTAATGGCTCTATTCCTGCTTCATTGGGGA 2082
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Key
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                                                                                                                                                                                           Local Si
hes 165;
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                                                                                                                                                                                                                     5.5%;
48.8%;
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                                                                                                                                                                                 Score 61.2; DB 1;
Pred. No. 2.1e-06;
0; Mismatches 173;
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2167 TTACTGAACTATTTTTGGGTAATAACTCTCTTAATGGCTCTATTCCTGCTTCATTGGGGA 2226

agcttgaacatttacagtatctagagctctacaaaaacaacatccaaggaactatacctt 475

356 tcactcgtgtggatttgggaaattcaaacctctctggacatcttgcgcctgagcttggga 415

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                                                                          PT Tomato gene Cf-5, confers resistance to Cladosporium fulvum - useful PT for production of transgenic plants resistant to pathogens e.g. PT tomato leaf mould C. fulvum in tomatoes
PS Disclosure; Fig 7; 75pp; English.

CC This sequence is a clone of the polynucleotide of the invention, which offer CC the invention is one of two tomato CF-5 gene variants, which offer CC tresistance against the pathogen resistance on a plant. The polynucleotide of CC can be produced by incorporating the gene into plant cells and CC regenerating plants from the cells; asexually or sexually produced CC offspring can also be subsequently produced. Expression of the gene in CC plant cells can confer pathogen resistance on a plant e.g. to tomatoe complementary to the gene or fragments of it, are useful in anti-sense techniques to reduce gene expression. The nucleic acids/polynucleotides CC are useful as hybridisation probes to identify other genes/fragments CC conferring pathogen resistance on plants e.g. Phytophthora resistance in CC potatoes. Homologies between Cf-5 and Cf-9 may be used to identify Sequence 4123 BP; 1253 A; 742 C; 725 G; 1403 T;
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     Matches
                       Query Match
Best Local :
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V14523;
20-MAY-1998
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20-NOV-1997.
08-MAY-1997; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF-5 pathogen resistance gene clone Hcr2-5D gene.
Tomato: CF-5 pathogen resistance gene; Cladosporium
tomato leaf mould; Phytophthora resistance; ss.
Lycopersicon pimpinellifolium.
Key
Location/Qualifiers
CDS
603. .3002
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24-SEP-1996; GE-019924.
09-MAY-1996; GE-0099881.
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untrivanthis K, Jones DA, Jones
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                   Similarity
   Conservative
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                 48.8%;
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Pred. No. 2.1e
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Gaps
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Search completed: June 23, 2000, 22:52:36 Job time: 40552 sec

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Title:
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Maximum DB
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Listing first 45 summaries
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1: /cgn2_6/ptodata/.

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4: /cgn2_6/ptodata/.

5: /cgn2_6/ptodata/.

6: /cgn2_6/ptodata/.

7: /cgn2_6/ptodata/.
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(without alignments)
524.282 Million cell updates/sec
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1106
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-567-680A-3
US-08-587-680A-3
US-08-587-680A-3
US-08-587-680A-3
US-08-238-163-3
US-08-238-163-1
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US-08-930-894-1
US-08-930-894-1
US-08-911-5772-0
US-08-911-5772-0
US-08-911-573-257-1
US-08-973-257-1
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US-08-475-891A-1
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US-08-846-338-13 US-08-508-786-2	US-08-909-965C-16 US-08-401-068-13	US-08-120-827-99 US-08-478-675-99 US-08-623-906A-16	US-08-724-394A-22 US-07-867-106-2	US-08-724-394A-20 US-08-724-394A-21	US-08-602-264A-1 US-08-859-201-1	US-08-883-515-1 US-08-618-911-3 US-08-618-911-5	US-08-189-256A-11 US-08-252-626A-1
Sequence 13, App. Sequence 2, Appl.		Sequence 99, Appl Sequence 99, Appl Sequence 16, Appl	Sequence 22, Appli Sequence 2, Appli	Sequence 20, App. Sequence 21, App.	Sequence 1, Appl: Sequence 1, Appl:	GENERAL INFORMAN Sequence 3, Appli Sequence 5, Appli	Sequence 11, Appl Sequence 1, Appli

ALIGNMENTS

```
Patent No. Journal C.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
TITLE OF SECUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Applic
Patent No. 5859339
                                                                                                                                                                                      REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0237.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/475,891A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                MOLECULE TYPE:
       OTHER INFORMATION:
OTHER INFORMATION:
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CITY: San Francisco
                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                               TOPOLOGY:
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join(1648..4383, 5178..5513)
NMATION: /product= "RRK-F"
NMATION: /note= "Xa21 Xanthomonas spp. disease
NMATION: resistance gene RRK-F from rice (Oryza
                                                                                                                                                                               linear
                                                                                                                                                   DNA (genomic)
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; OTHER INFORMATION: sativa) TUS-08-475-891A-1

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US-08-567-375-1
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Best Local Similarity
Matches 167; Conserv
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                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PATENTIA RE-BASE #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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                                                                                        APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Procedures and Materials for TITLE OF INVENTION: Disease Resistance in Plants
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ATTORNEY/AGENT INFORMATION:
NAME: Bastian Kerin '
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                                                                                                                                                                                    CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 04-DE
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                                       APPLICATION NUMBER: US 08/373,375 FILING DATE: 17-JAN-1995
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WENTION: Procedures and Materials for Conferring
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Song, Wen-Yuang
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US-08-567-375-1
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GENERAL INFORMATION:
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                              TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                       APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
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                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                          STREE: Two Embarcadero Center, Eighth Flor-
STREE: San Francisco
STATE: California
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                                                                                           COUNTRY:
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/product= "RRK.F"
/note= "Xa21 Xanthomonas spp.
resistance gene RRK-F from ric
(Oryza sativa)"
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Pred. No. 7.6e-07;
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; NAME/KEY: CDS; LOCATION: join(1648..4383, 5178..5513); OTHER INFORMATION: /product= "RRK-F"
; OTHER INFORMATION: /note= "xa21 xanthomonas spp. disease OTHER INFORMATION: resistance gene RRK-F from rice (Oryza OTHER INFORMATION: sativa)"
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Best Local Similarity
Matches 167; Conservi
Sequence 3, Application US/08567375
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
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                                                                                           3035 GCACCAACAAATTCAGTGGTTGGATACCA 3063
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CLASSIFICATION: 800
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TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 34,774
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                                                                                                                                                                                                                                                                                                                                                                                                                                    att---tacagtatctagagctctacaaaaacaacatccaaggaactataccttccgaac 481
                                                                                                                                                                  TGAGCGGTTCGATCCCATTGGCCATAGGAAATCTTACTGAACTTAATATCTTACTGCTCG
                                                                                                                                                                                                      tgaccggtccaatcctagagcactcacggcaatcccaagcctttaaagttgttgacgtct 661
                                                                                                                                                                                                                                               TTCCATCATCGTTGGGCAGGCTTAGAAACTTAGGCATTCTAGTCGCCTACGAAAACAACT
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Pred. No. 7.6e-07;
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Best Local Similarity
Matches 163; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NUMBER: WASHING FORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: U$\,2000.04567,375 FILLING DATE: 04-DEC-1995 CLASSIFICATION: 800
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ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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PRIOR APPLICATION NUMBER: US 60/004,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Guo-Liang APPLICANT: Song, Wen-Yuang APPLICANT: Szabo, Veronique
                                                            1279 GCCATTCTACTCGCCTACGAAAACAACTTGAGCGGTTCGATCCCGTTGGCCATAGGAAAT 1338
                                                                                                                                                                                                                              1159 AAGATCACAGGAAGCATTCCGAAGGATATTGGCAATCTTATTGGCTTACAACATCTCTAT 1218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                      442 ctctacaaaacaaccatccaaggaactataccttccgaacttggaaatctgaagaatctc 501
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562 ttgaagtototggtotttttacggottaatgacaacogattgacoggtocaatcotagag 621
                                                                                  502 atcagcttggatctgtacaaccaaccatcttacagggatagttcccactttcttgggaaaa 561
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product= "Xa-21"
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                            CTCTGCAACAACTTTCAGAGGGTCTCTTCCATCATCGTTGGGCAGGCTTAAAAAACTTA 1278
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Pred. No. 1.3e-06;
0; Mismatches 176;
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48.18;

Pred. No. 1.3e-06;
0; Mismatches 176;

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US-08-587-680A-3
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US-08-587-680A-3
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                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3921 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 08/373,375
EILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
EILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 60/004,645
EILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
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BEST APPLICATION DATA:
APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 17-JAN-19
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                                                                                                               MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                             LENGTH: 3921 base pairs
TYPE: nucleic acid
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                     LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product= "xa-21
                                                                  NAME/KEY:
                                                                                                                                     TOPOLOGY: 111
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REFERENCE/DOCKET NUMBER: 02
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Song, Wen-Yuang
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                       "Xa-21"
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Query Match

5.2%;

Score 57.4;

В 4;

Length 3921;

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GENERAL INFORMATION:
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                                                                                                             TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Processistance ...
TITLE OF INVENTION: Disease Resistance ...
PITLE OF INVENTION: Disease Resistance ...
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
Townsend and Townsend and Crew LLP
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APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                      REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                APPLICATION NUMBER: US 01
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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MOLECULE TYPE:
                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 06-JU
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                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94111-3834
                                                                                                                                                                                                                                 Bastian, Kevin L.
                                                    nucleic acid
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                                                                         5992 base pairs
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Song, Wen-Yuang
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                      linear
                                                                                                                                                    (415)
                                                                                                                                                                                                                                                                                                                                                     06-JUN-1995
DNA (genomic)
                                    single
                                                                                                                                    576-0300
                                                                                                                                                        576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Procedures and Materials for Disease Resistance in Plants
                                                                                                                                                                                                                                                                                          US 08/373,375
                                                                                                                                                                                                                                                                                                                                                                      US/08/475,891A
                                                                                                                                                                                                 02370-058910US
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; NAME/KEY: CDS
; LOCATION: Join(512.
; OTHER INFORMATION:
; OTHER INFORMATION:
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US-08-587-680A-24
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 163; Conserv
          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-POS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680 FILING DATE: 17-JAN-1996
                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1850 CTTACTGAACTTAATATCTTACTGCTCGGCACCAACAATTCAGTGGTTGGATACCATAC 1909
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PRIOR APPLICATION DATA:
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California
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Song, Wen-Yuang
Szabo, Veronique
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join(512..3149, 3993..4393)

;RMATION: /product= "RRK-B"

;RMATION: /note= "xa21 xanthomonas spp. disease

;RMATION: resistance gene RRK-B from rice (Oryza

;RMATION: sativa)"
                                                                                                                                                                                                                                                                                                                                                 USA
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Pred. No. 1.6e-06;
0; Mismatches 176;
                                                                                                                                                                                                                         Version
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; TOPOLOGY: linear; MOLECULE TYPE: CDNA (partial) US-08-587-680A-24
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SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                  US-08-238-163-3
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: BENETT
APPLICANT: LABAVIT
APPLICANT: POWELL,
APPLICANT: STOTZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.1%;
Best Local Similarity 49.0%;
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08238163 Patent No. 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
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COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CONDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                    TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
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                                                                                                                                                                                                                                                                                                                     BENNETT, Alan
                                                                                                                                                                                                                                                                                                  LABAVITCH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323
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STOTZ, Henrik
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29-SEP-1995
                                                                                                                                                                                                                                                                                                    John M
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Pred. No. 1.6e-06;
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US-08-238-163-3
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US-08-238-163-1
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                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08238163 Patent No. 5569830
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Best Local Similarity 50.3%;
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
SERVICE CHARACTERISTICS:
SERVICE CHARACTERISTICS
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
                                                                            APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
APPLICANT: POWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                               CORRESPONDENCE
                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          629
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SOFTWARE: Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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(415) 543-5043
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Townsend and
                               ADDRESS:
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Townsend Khourie and
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Pred. No. 6.7e-06;
0; Mismatches 181;
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RESULT 10
US-08-567-375-15
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; LCCATION: 1..1058
; OTHER INFORMATION: /standard_name-
US-08-238-163-1
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Best Local Simi
Matches 122;
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REGISTRATION NUMBER: 34,774
REFERENCE_MOCKET NUMBER: 230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      Sequence 15, Patent No. 5
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CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
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MEDIUM TYPE: Floppy disk
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CITY: San Francisco
STATE: California
COUNTRY: US
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STRANDEDNESS: .single
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Similarity 51.5%;
                                                                                                                                                                                                         Application US/08567375
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34..1023
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Pred. No. 1.2e-05;
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Townsend and Townsend and Crew LLF

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WESULT 11
US-08-473-553A-1
; Sequence 1, Application US/08473553A
; Patent No. 5859338
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REGISTRATION NUMBER: 34,774
REFERENCE, DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
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APPLICATION NUMBER: US 01
FILING DATE: 07-JUN-1995
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APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
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MEDIUM TYPE: Floppy disk
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CITY: Sa
STATE: C
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                                                                                                                                                                                                                                                                          153 TGGACTCGAGTAGAAACAACTTCTCTGGCACAATCCCTCCTCAGATTGGTAACTGTCTTT
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                                                                                          333 C 333
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                                                                                                                                                  273 CTCAAATTCACATCTTAAATTACATCAATATTTCCTGGAATCACTTCAACGAGAGCCTTC 332
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                                                                                                                                                                                                                                                                                                                                     93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                 33 CTGGTGCACTTCCTAGTGCTTTTGGAAACTATTCAGGGCTGAAGAATCTTGTGTTAACTG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                GAAATGGTTTCTCAGGTGATATCCCTTCTGATATTGGCAGACTAAAGAGCATCTTAAAGC 152
                                                                                                                                                                                                              CCTTAACTTACTTGGATTTGAGCCAAAATCAACTTTCTGGTCCTATCCCAGTTCAAATTG 272
                                                                                                                                                                                                                                                                                                    tggatctgtacaacaacaatcttacagggatagttcccactttcttgggaaaattgaagt 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                              3422
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Query Match
Best Local Similarity 47.0
Matches 151; Conservative
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TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
DATH TOTAL NUMBER. US //08/173 ES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Plant Clavatal Nucleic Acids, TITLE OF INVENTION: Transformed Plants, and Proteins
                                                                                                                                                                                                                                                                                                                                                                                            3482 GGGAGAACAATTTCACGTTACAATTACCGGCGAATCTTGGCCGGAACGGGAATCTAATAA 3541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                               3542 AGCTTGATGTCTCTGATAATCATCTCACCGGACTTATCCCCCAAGGACTTATGCAGAGGTG
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626 cacggcaatcccaagccttta 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Flehr, Hohbach, Test, STREET: Four Embarcadero Center,
                                                                                  gcttggatctgtacaacaatcttacagggatagttcccactttcttgggaaaattga 565
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                                                                                                                                                                                                                                                                                                            TCTACGGACAAATACCAGAGGCCATCGGAGAATTACCAAAACTCGAAGTCTTCGAAGTAT
                                                                                                                                                                                                                                                                                                                                                 tototggacatottgcgcctgagcttgggaagcttgaacatttacagtatotagagctct 445
                                                               AGAAATTAGAGATGTTAATTCTCTCTAACAACTTCTTCTTTGGTCCAATTCCAGAAGAGC
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2434..5037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.48;
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Pred. No. 0.00033;
D; Mismatches 170;
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Suite 3400
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3662 TIGGTAAATGCAAATCCTTAA 3682

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RESULT 12
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Patent No. 5670367
                                                                                                                                                                                                                                                                            Query Match 4.4%; Score 48.6; DB 1; Length 7218; Best Local Similarity 3.5%; Pred. No. 0.00047; Matches 12; Conservative 196; Mismatches 135; Indels 0
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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APPLICANT: DORNER
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: RECOMBINANT
                                                                 1233
NUMBER OF SEQUENCES:
                                                                                                                                                                       108
                                                                                                                                                                                                                                           48 ccctaattttgctttctcctctttgttcagaaaattttcccttttactctcaaaattccttt 107
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                             cgaaggagatgctctctacgctcttcgccggagtttgacagatccagaccatgtcctcca
                                                                 gctcttcgcagcttcgttaaccctaaccttagctttgattcacctggtcgaagcaaactc 227
                                                                                                                                                                    tcgatttccctctcttaaacctccgaaagctcacatggcgtctcgaaactatcggtggga 167
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22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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5169835-11
;Patent No. 5169835
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Best Local Similarity 55.2
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US
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TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS
NUMBER OF SEQUENCES: 48
               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                             SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,649
FILING DATE: 06-JUN-1994
                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS: ADDRESSEE: Sally A.
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TITLE OF INVENTION: Nucleotide Sequences Coding An
TITLE OF INVENTION: Endopolygalacturonase Inhibitor
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                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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COUNTRY: US
ZIP: 80303
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CITY: E
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FILING DATE:
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Salvi, Giovanni
Albersheim, Peter
                                                                                                                                                                                                                                                                                                                                                                                          Darvill, Alan
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06-DEC-1991
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55.2%;
               IT RM 91A 000915
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                                                                                US/08/244,646
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                                                                                                                    Version
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FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A.

APPLICATION NUMBER: WO POSITION DATE: 04-DEC-1992

WO PCT/IT/00158

PRIOR APPLICATION DATA:

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US-07-867-106-2/c
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US-08-244-646-16
                                                                                                                                                                  Sequence 2, Application US/07867106 Patent No. 5389526 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (303)499-808
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 19-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Pha:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                               CTCCCCAACCTCGTAGGAATCACATTCGACGGCAACCGAATCTCCGGCGCCCATCCCCGAC
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Pred. No. 0.025;
0; Mismatches 127;
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Search completed: June 23, 2000, Job time: 40238 sec

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; LOCATION:
US-07-867-106-2
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Best Local :
                                                                                                                                                                                                                                                                                Matches
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ETILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU J/7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-588-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                        5500
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                          1088 aaaaaaaaaaaaaaa 1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel
                                                                                                                                         968
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Local Similarity 47.3%;
es 121; Conservat:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                          aggtctgtatgtaaaatttctaaatgcgattttcgcttactgtaatgttcggttgtggga 1027
                                                                                                                                                                                     aaaacaaaaaaatgaagaatcgaatcggtaatatcatctggtctcaattgagaacttcg 967
                                                   ttctgagaagtaacatttgtattggtattggtatcaagttgttctgccttgtctgcaaaaa 1087
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2378..5038
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Database :
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Listing first 45 summaries
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Maximum DB seq length: 1000000
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Perfect score:
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(without alignments)
723.220 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.

Score

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AI92868 469 bp mRNA EST 08-SEP-1999 701493826 A. thaliana, Ohio State clone set Arabidopsis thaliana CDNA clone 701493826, mRNA sequence. AI92868 AI992868 1 GI:5839773 EST. thale cress. Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 469) Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D., Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P., Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D., Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C., Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobriga,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and	ALIGNMENTS	545 548 5497 54	21.8 305 25 N65416 21.7 569 59 A1775448 21.6 667 74 AW188847 21.4 676 74 AW220075 21.1 430 79 AW307218 20.9 515 79 AW3079515 20.6 619 64 AW040482 20.5 304 36 T21150	23.6 71.4 64 AW030188 23.6 714 64 AW030188 23.4 334 23 H37195 22.6 599 63 AW011134 22.5 695 64 AW038168 22.0 599 74 AW219797 21.9 522 46 AI441759 21.8 637 80 AW350549		31.1 401 37 30.2 534 33 30.2 534 42 29.6 442 42 29.6 336 20 29.6 336 42 28.6 350 42 28.7 364 42	Length DB ID 469 63 A1992868 A1992868 7014 447 23 H36800 H36800 14929 556 22 B80008 B80008 1632
Oy 462 aggaactataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtacaa 521			Qy 102 tccttttcgatttccctctttaaaccttccgaaagctcacatggcgtctcgaaactatcg 161	Query Match 36.9%; Score 407.6; DB 63; Length 469; Best Local Similarity 93.8%; Pred. No. 3.7e-85; Matches 450; Conservative 0; Mismatches 19; Indels 11; Gaps 2; Qy 42 acgtaaccctaattttgctttctcctctttgttcagaaaattttccctttactctcaaat 101	/Organism="Arabidopsis thaliana" //db_xref="taxon:3702" //clone="701493826" //clone=1ib="A. thaliana, Ohio State clone set" //clone=1ib="A. thaliana, Ohio State clone set" //note="cDNA library was made from selected clones from the library was made from selected clones from the library was made from selected clones from the library was made from selected clones from the library was made from selected clones from the librar	. 0 1 1 1 2 4	Hanson,D. TITLE Arabidopsis thaliana Gene Expression MicroArray JOURNAL Unpublished (1999) COMMENT On Dec 20, 1995 this sequence version replaced g1:1135328.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

RESULT 1
A1992868
LOCUS
DEFINITION

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BASE COUNT
ORIGIN
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MEDLINE
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Best Local Similarity
Matches 418; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaaaattttccctttactctcaaattccttttcgatttccctctcttaaacctccgaaag 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctagagctctacaaaaacaacatccaagg 464
                                                                                                                             ggagtttgacagatccagaccatgtcctccagagctgggatccaactcttgttaatcctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCAACTTCAATAAAGGGG-AACCAACGTAACCCTAATTTTNCTTTCTCCTCTTTGTTCA 59
                                                                             attcaaacctctctggacatcttgc-gcctgagcttgggaagcttgaacatttacagtat 435
                                                                                                                                                                                                         GGAGTTTGACAGATCCAGACCATGTCCTCCAGAGCTGGGATCCAACTCTNGTTAATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAAATTTTCCCTTTACNCTCAAATTCCTTTTCGATTTCCCTCTTAAACCNCCGAAAG
                                                       ATTNAMACCTCTNTGGACATCTTGCGGCCTNAGGTTGGGGGAGNTTGAACATTTTCAGTAT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant physiol. 106, 1241-1255 (1994)

95148729

Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRI, Michigan State University, Plant Biology Bldg., E.
Lansing, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis.

1 (bases 1 to 447)
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primer: T7 dye primer.
    Location/Qualifiers
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a 115 c 83 g 126 t 17 others
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/clone="179A22T7"
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93.1%;
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                                                                                          agcttggatctgtacaacaaccaatcttacagggatagttccccactttcttgggaaaattg
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Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
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MSU-DOE-PRL, Michigan State University, Plant
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MSU-DOE Plant Research Laboratory
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/clone_lib="Lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA."
/note="Vector: lambda Zip-Lox; The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA."
/note="Vector: lambda Zip-Lox; The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA."
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/strain="var columbia"
/db_xref="taxon:3702"
/clone="187H5T7"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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31949 Lambda-PRL2
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MSU-DOE Plant Research Laboratory
Michigan State University
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Contact: Ti
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                                     /note-"Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRU's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using
            inserts were directionally cloned with oligo dT primed cDNA. " 105 c 78 g 99 t 16 other
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/strain-"var columbia"
/db_xref-"taxon:3702"
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                                                                                                                                                                                                                                                              Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                               Lansing,Mi
Tel: 517-353-0854
                                                                                                                                                                                                                                                                                                                                 On May 18, 1995 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis.
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                                                                                                                                                                                             Fax: 517-353-9168
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                                                                                                                                                                          22313tcn@ibm.cl.msu.edu
                                                      /organism="Arabidopsis/strain="var columbia"/db_xref="taxon:3702"
                  /clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal;
                                        /clone="305G1T7
                                                                                                                                    Location/Qualifiers
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Arabidopsis thaliana
Arabidopsis viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; endicotyledons; core
euphyllophytes; Spermatophyta; Magnollophyta; endicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.

1 (bases 1 to 336)

Newman, T., deBruijn, F.J., Green, P.,
MCIntosh, L., Ohlrogge, J., Raikhel, N
Retzel, E. and Somerville, C.
Genes galore: a summary of methods
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EST.
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Lambda-PRL2
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                                        Green, P., Ko
Raikhel, N.,
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sequence.
AI100481
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EST.
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The sequence entry for this EST
is being submitted in the sense
Seq primer: M13-21
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Tel: 517-3
                                                            34856
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Fax: 517-353-9168
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3 others
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/strain="var columbia"
/db_xref="taxon:3702"
/clone="179J19xp"
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Pred. No. 9.1e-68;
0; Mismatches 3
                                                             thaliana
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orientation
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atcatctggtctcaattgagaacttcgaggtc--tgtatgtaaaatttctaaatgcgatt
                                                                                                                                           tttgctcacattcctttacagaactttgagaacaacccgagattgg--agggaccggaat 760
                                                                                                                                                                                                                                                                                                                                                                                                TAAAGTTTNTTGGATTCTNCAGCCAINGTTTGTGTGGAACAATCCCCAACAAACGGACCT 60
                                                               ttatgtaataagtatatatgtagtaaaaacacaaaaaaatgaagaatcgaatcggtaat
                                                                                                                                                                                                                                 TACTCGGTCTTGCAAGCTACGACACTAACTGCACCTGAAAAAATTGGCAAAACCTGAAAA
                                                                                                                                                                                                                                                    tactcggtcttgcaagctacgacactaactgcacctgaaacaactggcaaaacctgaaaa 820
                                                                                                                                                                                                                                                                                                                 397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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The sequence entry for this EST has been reverse complimented
is being submitted in the sense orientation.
Seq primer: M13_Universal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //Clone_lib="Lambda-PRL2"
//Clone_lib="Lambda FRL2"
//note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
//note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
//note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
//note="Vector: lambda Zip-Lox; The mRNA sources were 1) 7

quantities of 4 pools of mRNA. The mRNA sources were 1) 7

day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)

same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA.

82 c 90 g 132 t 3 others
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/strain="var columbia"
/db_xref="taxon:3702"
/clone="90J7XP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.6%;
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Pred. No. 1.5e
0; Mismatches
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Raikhel,N.,
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,S., Thomashow,
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93
                                                      atcaagttgttctgccttgtctgc
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                                                                                                                                                                         AGAACAACCCGAGATTGGAGGGACCGGAATTACTCGGTCTTGCAAGCTACGACACTAACT
                                                                                                                                                                                     agaacaacccgagattggagggaccggaattactcggtcttgcaagctacgacactaact 790
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acaaaaaaatgaagaatcgaatcggtaatatcatctggtctcaattgagaacttcgagg 970
                                                                                                               GCACCTGAAACAACTGGCAAAACCTGAAAATGAAGAATTGGGGGGGTGACCTTGTAAGAAC
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ATTS3221 Versailles-VB
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratoire de Biologie Cellulaire
Route de Saint-Cyr, 78026 Versailles
Email: thierry@versailles.inra.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Arabidopsis thaliana transcribed genome: Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                           89
                                                                                                                                                                                                                                                                                                                                                                          /Clone_lib="Versailles-VB"
/tissue_type="whole seedlings"
/tev_stage="in vitro-grown etiolated seedlings,5 days old"
/dev_stage="in vitro-grown etiolated seedlings,5 days old"
/note="Vector: pBluescript"
/note="Vector: pBluescript"
62 c 65 g 119 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone-"VBVDH02"
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                                                                                                                                                                                                                                                                                                    29.68;
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Pred. No. 2e
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Mismatches
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                                                                                                                                                                                                                                                                                                                Length
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                                                                                     783
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                                                                cactaactgcacctgaaaccaactggcaaaaacctgaaaaatgaagaattggggggtgacctt 842
CACTAACTGCACCTGAAAAAATTGGCAAAACCTGAAAATGAAGAATTGGGGGGGTGACCTT 120
                                                                                                                                                                                                                 346;
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33806 Lambda-PRL2 Arabidopsis thaliana
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The sequence entry for this EST
is being submitted in the sense
Seq primer: M13-21.
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1 (bases 1 to 360)
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Tel: 517-353-0854
Fax: 517-353-9168
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Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 5, 1995 this sequence version replaced gi:797715
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                                                                                                                                                                                                                                                                                                                                       /notes vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated eticlated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA.

16 a 60 c 77 g 105 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis
/strain="var columbia"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Lambda-PRL2"
                                                                                                                                                                                                                                 28.6%;
95.6%;
                                                                                                                                                                                                            Score 316; DB 42;
Pred. No. 8.3e-64;
0; Mismatches 12;
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cDNA clone 90J7XP 3', mRNA
                                                                                                                                                                                                                                                        Length 360;
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MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                   Fax: 517-353-9168
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                                                                                                                                                                                                                                                                                                                                              il: 22313tcn@ibm.cl.msu.edu
primer: T7 dye primer.
                 98
       /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and sliiques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using ollgo dT primed cDNA. "

85 c 67 g 89 t 14 others
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/strain="var columbia"
/db_xref="taxon:3702"
/clone="179J19T7"
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Raikhel, N.,
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., Somerville,S., Thomashow,M.,
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McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomash
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from the second partial sequencing of anonymous Arabidopsis cDNA in physiol. 106, 1241-1255 (1994)
E. 95148729
On May 5, 1995 this sequence version replaced g1:797711.
Contact: Thomas Newman
MSU-DDE Plant Research Laboratory
Michigan State University, Plant Biology Bldg.,E
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                                                                                                                 Email: 22313tcn@ibm.cl.msu.edu
The sequence entry for this EST
is being submitted in the sense
Seq primer: M13-21.
                                                                                                                                                                 Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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/organism-"Arabidopsis
/strain-"var columbia"
/db_xref-"taxon:3702"
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                                                                    Laboratoire de Biologie Cellulaire
Route de Saint-Cyr,78026 Versailles
Email: thierry@versailles.inra.fr.
Location/Qualifiers
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/organism="Arabidopsis thaliana"
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33803 Lam
        Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcneibm.cl.msu.edu
The sequence entry for this EST has been reverse
is being submitted in the sense orientation.
Seq primer: M13-21.
                                                                                                                                          On May 5, 1995 this sequence version
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                     Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow, Retzel,E. and Somerville,C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA cleant Physiol. 106, 1241-1255 (1994)
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/tissue_type="whole seedlings"
/dev_stage="in vitro-grown etiolated seedlings,5 days
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                                                                               Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
On May 8, 1995 this sequence version replaced gi:801143 Contact: Thomas Newman
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Tel: 517-353-9168
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
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Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                    AW443205 608 bp mRNA EST EST308135 tomato mixed elicitor, BTI Lycopersicon clone cLET43M10 5', mRNA sequence.

AW443205
                           Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

1 (bases 1 t
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10; Conservative
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86 c 59 g 89 t 13 others
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/strain="var columbia"
/db_xref="taxon:3702"
/clone="179J1177"
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                                                                    cgattgaccggtccaatcctagagcactcacggcaatcccaagcctttaaagttgttgac
                                                                                                                    ACAATTCCTACTTCACTTGGAAACCTGAAAAACCTTGTTTTCTTGCGTCTAAATGATAAC
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Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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100 Jordan Hall, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 68.7
95; Conservative
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/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
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/clone=lib="tomato mixed elicitor,/
/tlssue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue_MRF/"
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68.7%;
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Pred. No. 4.8e-57;
0; Mismatches 180;
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1 (bases 1 to 1063)

De, V.S. Schmidt, E.D., Van, H.G. at PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;

CIBA GEIGY AG (CH)
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De, V.S., Schnidt, E.D., Van, H.G. and
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
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Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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1 (bases 1 to 2089)

1 (bases 1 to 2089)

De, V.S., Schmidt, E.D., Van, H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;
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GGTTCGATTCCAGAAACACTAGGCAACCTGACTAATCTCATCAGCTTGGATCTCTGGGAC
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                                                        ggaactataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtacaac 484
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Sorghum,
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Sorghum bicolor leucine-rich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hipskind, J.D., Nicholson, R.L. and Goldsbrough, P.B. Isolation of a cDNA encoding a novel leucine-rich Sorghum bicolor inoculated with fungi and the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
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/db_xref="GI:1710124"
/translation="MAPOFAAAGFLTGLLALATFASCNTEGDILYKQRLAWEDPNNVL/CYANDSLATION TELYGNGL GSWNSTLANPCTWFHVTCNNNNFVIRVDLGNAGISGPLLPDLAEIQNLQYIELYGNGL NGSIPETLGNLTNLISLAWDNLTGEIPTTLGSVSTLRYLRLYQNNLTGPIPSSEGN LTSLLESKLQENSLSGAIPASLGNIKALQFSRLNDNMLTGTVPSKSFPLSTFGNLTEL NTDRNNLDGTRTSSGLRVTAIIQDALKTA"
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/note="leucine-rich repeat-containing extracellular
glycoprotein; contains six N-glycosylation sites
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U93048.1 GI:2
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A leucine-rich repeat containing receptor-like kinase marks somatic plant cells competent to form embryos Development 124 (10), 2049-2062 (1997)
97313247
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Daucus carota somatic
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Direct Submission
Submitted (12-mAR-1997) Molecular Biology, Agricultural University
of Wageningen, Dreyenlaan 3, Wageningen 6703 HA, The Netherlands
Location/Qualifiers
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Schmidt, E.D.L., Guzz
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SNNRLSGPVDDNGSFSLFTPISFANNLHCGPVTGRPCDGSPPSFPPPFIPSTYQP
PGQNGPTGALAGGVAAGAALLFAAPAMAFAWMRRKKPREHFDVPAEEDDFUHLGOLK
RFSLRELQVATDTFSTILGRGGFGKVYKGRLADGSLVAVKRLKEERTPGGELGPGTEV
EMISMAVHRNLLRLGGCMTPTERLLVYPYMANGSVASCLRERGDSEPPLDWPTRKRI
ALGSARGLSKLHÜHLDPKITHENGANITLLDEFEAVVGDFGLARLMVSKUTBYTGT
ALGSARGLSKLHÜHLDHCJPKAANITLDEEFEAVVGDFGLARLMVSKUTBYTGA
VRGTLGYIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDVMLLDWV
KSLLKKEKKLEMLVDPDLENNYIDTEVEGLIQVALLCTQGSPMERFMSEVVRMLEGDG
LAEKMDEMGKYEVIHGDVELAPHTSEWILDSTDNLHAFELSGPR
A 347 C 407 g 495 t
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/protein_id-"AAB61708.1"
/db_xref-"G1:224911"
/translation-"MNRNSINIINYMQFTDAYLDKYGVLMTLELYSNNISGPIPSDLG
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Score 101.8; DB 8; Pred. No. 5.1e-15; 0; Mismatches 162;
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10, Vas., Schmidt, B.D., Van, H.G. and Hecht, V.F.

PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20.NOV-1997;

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RFSLRELQVATDTFSTILGRGGFGKVYKGRLADGSLVAVKRLKEERTPGGELQFQTEV
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2 (bases 1 to 4604)

Tornero, P., Mayda, E., Gomez, M.D., Canas, L., Conejero, V. and Vera, P. Characterization of LRP, a leucine-rich repeat (LRR) protein from tomato plants that is processed during pathogenesis

Plant J. 10 (2), 315-330 (1996)
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ELYKNNIQGTIPKELGNLKSLISLDLYNNNISGTIPTSLGNLKNLVFLRLNDNKLTGE
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/gene="LRP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GGTTTGTTGGCAGTTGTTCTTGCTGTAGCTGTGGCTGTAAAGGGGGAATTCAGAAGGGGAT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 gcttcgttaaccctaaccttagctttgattcacctggtcgaagcaaactccgaaggagat 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        actcgtgtgga 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccaactcttgttaatccttgtacctggttccatgtcacctgtaaccaagacaaccgcgtc 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gctctctacgctcttcgccggagtttgacagatccagaccatgtcctccagagctgggat 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTTTGTACGCCCTTCGCCGGAGCTTATCTGACCCGGGTAACGTGTTACAGAGCTGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTCGTGTGTA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCANATCTTGTTAACCCTTGTACCTGGTTTCATGTCACTTGCAACGGAGATAATCAAGTT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132;
                                       Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B., Ronning,C.M., Koo,H., Fujil,C.Y., Utcrback,T.R., Barnstead,M. Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome III BAC F9F8 genomic sequence unpublished
                                                                                                                                                                                            Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                 ATACO09991 101284 bp DNA PLN 08-OCT-1999 ATACO09991 thaliana chromosome III BAC F9F8 genomic sequence,
      Lin,
                                                                                                                                                                                                                                                                                                                                                                  complete sequence.
                                                                                                                                                                          Arabidopsis.
                                                                                                                                                                                                                                                                                                                        AC009991.3 GI:6016677
                                                                                                                                                                                                                                                                                thale cress.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3153. .4282
/gene="LRP"
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/gene="LRP"
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/gene="LRP"
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=6
758 c
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3153. .42
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3000. .301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=3
2928. .29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number=3
2709. .29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number=2
2565. .27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number=5
4283. .>4604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="LRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2453.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="LRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene-"LRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="LRP"
                          1 to 101284)
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Pred. No. 9.9e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                            Barnstead, M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.cbs.dtu.dk/netbgene/cbsnetbgene.html)) searches of the complete sequence against a peptide database and the Arabidopsis EST database at TICR (http://www.tigr.org/tdb/at/at.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity. That are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy. http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://genome.wustlnigton.edu/RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted exons by GRAIL are annotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Dr.
Rockville, MD 20850, USA
e-mail: xlin@tigr.org
BAC clone F9F8 is from Arabidopsis chromosome III and is near the
molecular marker g4547.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-SEP-1999) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org 3, (bases 1 to 101284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medical Center Dr., Rockville, MD 20850, USA On Oct 8, 1999 this sequence version replaced gi:5902413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (08-OCT-1999) The Institute for Genomic Research, 20850. USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of from arthur.epm.cornl.gov), Genefinder (Phil Burge, Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xiaoying Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Address all correspondence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone
                                                                                                                                                                                                                                                                                                                                                                /note-"exon predicted excellent_shadowexon" 355. .594
/note="exon predicted by xgrail, complement(2090. .2250) /note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="exc
124. .259
                                                                                                                              complement(1516...1694)
/note="exon predicted b
excellent_shadowexon"
                                                                                                                                                                                                                                                                                /note="exon predicted 854. .973
                                                                                                                                                                                                                                                                                                                          /note="exon predicted by 672. .752
                                                                  /note="exon predicted by 1747. .1838
                                                                                                                                                                                            /note="exon predicted by marginal_shadowexon"
                                                                                                                                                                                                                                        /note="exon predicted by xgrail,
complement(1182. .1357)
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="exon predicted by xgrail, complement(347. .408)
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77. .108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon predicted by xgrail,
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quality excellent"

quality

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quality excellent"

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excellent"

excellent"

quality good_shadowexon"

CDS

mRNA

gene

quality marginal"

.14582,

quality

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misc_feature
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/rpt_family="(CAAA)n"
                                                                                                                                                                                                                                                          /gene-"F9F8.3"
/notee"similar to leucoanthocyanidin dioxygenase
/notee"similar to leucoanthocyanidin dioxygenase
GB:BAA20143 [Perilla frutescens]"
complement(join(9426. .9674,10198. .10528,11098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLSVSFYFGARLNRNERKRLFSLINDLPTLFDVVTGRKAMKDNRPSSDSGSKSRNGTK
RSIDGOTKSSTPKLMEESYEEEEEEEDEHGDTLCGSCGGHYTNEEFWICCDVCERWYHG
KCVKITPAKAESIKQYKCPPCCAKKGRQ"
complement(7717. .7760)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative nucleic acid binding protein"
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/db_xref="G1:6016679"
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/translation="MAAAAVSSNPRTVEEIFKDYSARRAALLRALTKDVDXSLVAVHSDCW
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5589. .7932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSMPTEFADDSPYDLVSADGKQTVNSSEWTYFWEEQWD"
complement(5513..5597)
/rpt_family="(GA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /PICCEID_Id-"AAF01505.1"
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/DICCEID_Id-"AAF01505.1"
/DLAXTEFT"GI:6016678"
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YYGWNSSRALEVVDQVFFKDAAVQPSLVIVYFGGNDSMAPHSSGLGPHVPLTEYVDNM
KKIALHILQSLSDFTRIIFLSSPPVDEAKVRQNQSPYLSEVIRINDLCKIYSDACVELC
QELGLEVVDLFSTFQKADDWKTVCFTDGIHLSAQGSKIVAGEILRVVKEAEWHPSLHW
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/note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                          complement(<9426. .>11865)
/gene="F9F8.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(GAAAA)n"
8515. .8572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to nucleic acid binding protein Alfin-1
GB:AAA20093 [Medicago sativa]"
join(5696. .5795,5897. .5929,6013. .6235,7264. .7387,
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VKLGGRLMTILSSNIGIRAEQUQEAFGGEDVGACLRVNYYPKCPQPELALGLSPHSDP
VKLGGRLMTILSSNIGIRAEQUQEAFGGEDVGACLRVNYYPKCPQPELALGLSPHSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (7810. .7847)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="exon predicted excellent_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F9F8.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F9F8.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )oin(5589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="F9F8.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oin(3215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="similar to unknown protein GB:AAC27167 [Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oin(3070
                                                                                                                                                                                                      /gene="F9F8.3"
/codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                    /gene="F9F8.3"
                                                                                                                                                                                                                                                                                                                                                                                                     olement(join(<9426. .9674,10198. .10528,11098.
91. .>11865))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family="(CAT)n"
ement(7810
                                                                                                                                                                                                                                                                                                                                                                                                                                                         family="(TAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3070. 3325,3565. 3642,4094. 4655,4800. >5013)
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.4655,4800. .5013)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5795,5897. .5929,6013. .6235,7264. .7387,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTACAGGTTGATTCCAATAAGCTCAGTGGAAATGTTCCCCATCTCACTACTGAATTTGA
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                                                                                                                                      AC021198
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/note="exon predicted by complement(13742...13788)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="aaf01508.1"
/db_xref="G1:6016681"
/db_xref="G1:6016681"
/translation="mamfulvesecgirplpriyTtprsnelsninkerpslssssykts
ssplseglnsrdgetrnwalnvstplitplfesspleednkorfdpappfenladir
aaipkikowyknewkslsyvvrdulkssilvpradaaaxtunwivmelywladgetmymalfvb
lghdcghgsesddpklinsvyohilhessilvprhgwrishryhlonhghyendeswhph
sekiyntldkptrefertlplvmlaypfylwarspgkkgshyhpdsdlflpkerkdvl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="(GA)n"
12824. .12836
/note="exon predicted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(13988. .14179,14261. .14398,14502. .14582, 14576. .14861,14941. .15033,15124. .15190,15272. .15361,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="identical to omega-3 fatty acid desaturase,
chloroplast precursor GB:P46310 [Chloroplast Arabidopsis
thaliana]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(13822. .16380)
/gene="F9F8.4"
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/gene="F9F8.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="omega-3 fatty acid desaturase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F9F8.4"
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Pred. No. 26
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Length 101284; Indels

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gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 acctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatctagagc 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 8.3%;
Local Similarity 54.1%;
                                                                                                                                                  cactcacggcaatcccaagccttaaagttgttgacgtctcaagcaatgatttgtgtggaa 644
                                                                                                                                                                                                                                                              tgaagtototggtotttttaoggottaatgacaacogattgacoggtocaatcootagag
                                                                                                                                                                                                                                                                                                                                                                             tcagcttggatctgtacaacaatcttacagggatagttcccacttctttgggaaaat 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAGTAACAACATACCGGTTCAATTCCTTCCTTAGGAAATCTCAAGAATTTGA 2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              totacaaaaacaacatocaaggaactatacottccgaacttggaaatctgaagaatctca 464
  TCATTCC
                                                        caatccc 651
                                                                                                              CCTTCGGAAATCTCAAGAACTTGACGTATCTTTATCTTTACCTGAATTATTTAACTGGTG 2765
                                                                                                                                                                                                                                TGGAATCGATGATTTACAGTTGAATAACAACATACCTTACCGGTTCAATTCCTTCTT 2705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-FEB-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA on Feb 11, 2000 this sequence version replaced gi:6693723. The sequence is of BAC F14D7 from Arabidopsis thaliana chromosome 1. The sequence does not represent the sequence of the entire insert of this clone. It is shorter by 6954 bp because we submit only the unique sequence of the clone. However, in order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide small overlaps (200 bp) between overlapping sumbitted clones. The 5' end of this sequence overlaps by 200 bp to the 3' end of the sequence of the clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-JAN-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA 3 (bases 1 to 81513)
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Liu,S.X., Sakano,H., Yu,G., Lee,J.M., Lenz,C., Pham,P., Torium,Chin,C., Chiou,J., Choi,E., Chung,M., Gonzalez,A., Howng,B.,
Liu,A., Vaysberg,M., Altafi,H., Brooks,S., Buehler,E., Chao,Q.,
Conn,L., Conway,A.B., Hansen,N.F., Johnson-Hopson,C., Khan,S.,
Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,
Southwick,A., Davis,R.W., Ecker,J.R., Federspiel,N.A. and
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
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Pred. No. 5.6e-10;
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                                                                                                                                                                                                                                            http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tlgr.org/tdb/at/at.html).

Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/krNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted exons by.GRAII are annotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin,X. and Kaul,S.

Direct Submission
Submitted (14-OCT-1999) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org
3 (bases 1 to 134402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin'X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome I BAC F1M20 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete sequence. AC011765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATACO11765 134402 bp DNA PLN 08-DEC-1999 ATACO11765 thaliana chromosome I BAC F1M20 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous if from arthur.epm.ornl.gov), Genefinder (Phil Green, University Washington), Genscan (Chris Burge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAC clone F1M20 is from Arabidopsis chromosome I and is near the molecular marker m1425.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Dec 8, 1999 this sequence ve Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (08-DEC-1999) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
On Dec 8, 1999 this sequence version replaced g1:6102640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rockville, MD 20850, (e-mail: xlin@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research 9712 Medical Center Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis.
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/db_xref="taxon:3702"
/chromosome="I"
                                                                                                                                                                       /organism="Arabidopsis thaliana
                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                     .134402
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to dolichyl-phosphate mannosyltransferase polypeptide 2 08:450365 [Homo sapiens] (regulator of dolichol phosphate-mannose synthesis: EMBO J 1998 Sep 1;17(17):4920-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HKRGTASSALVSQYFTTKPFACDPSSLPIYPPSKEIDTKHRDEAARSVISFIT" complement(4069. .4131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNVAGEAIHGWVPLRSDAFEKLEKIGQGTYSNVFRAVETETGRIVALKKVRFDNFEPE
SVKFMAREILILRRLNHPNIIKLEGLITSKLSCNIQLVFEYMEHDLTGLLSSPDIKFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative protein kinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="exon predicted by xgrail, quality marginal" complement(join(<1655. .1777,1908. .2135,2258. .2581, 2679. .2963,3052. .>3429))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="exon predicted by xgrail, quality good_shadowexon"
complement(1509..1530)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="exon predicted by xgrail,
complement(1356. .1475)
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complement(744. .1286)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="exon predicted by xgrail, quality excellent"
complement(393. .453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(<4608. .>4974)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon predicted by xgrail, quality excellent"
complement(join(<4608. .4760,4885. .>4974))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKPLTSRVYTLWYRPPELLLGATDYGASVDLWSVGCVFAELLLGKPILKGKTEVEQLH
KIFKLCGSPPEDYWKKSKLPHAMLFKPQQTYDSCLKETLKDLSETEINLIETLLSIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(<1655. .>3429)
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                                                                                                                                       complement(5342. .7603)
/gene="F1M20.3"
                                                                                                                                                                                                                                                                                                                     /note="exon predicted by xgrail, quality excellent"
complement(<5342. .>7603)
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PQDYAILVPVFAGIALLSLISVFIGMVMLKSKKKKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPQIKCYMKQLLSGLDHCHSRGVMHRDIKGSNLLLSNEGILKVADFGLANFSNSSGHK
                                                                                                                                                                                                                                                                 complement(<5342. .>7603)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative dolichyl-phosphate mannosyltransferase
oolypeptide 2"
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                                                                                                                                                                                                                                                                                                                                                                            .ement(5111
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20.2"
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CDS

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misc_feature
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//Leasi atton="MAATAVAGDSLDSDREVILLSLKSYLESRNPQNRGLYTEWKMENQ
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VXASNVLLDKHGNARVTDEFGLARLFWGDSHVSTVIAGTIGVAPEXGQTWQATTRGD
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/noq2..>14231
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ELSSGYFDVASNIFSIVARDKYKEVLVLPSVALKVVOŒAIRIVLEVVESPHFSKISHS

CRSGRGRASALKYINNISKRSDWCFFUSLIKKLDVSVERULSYMEERVEDSSLSILL

RSMFEARVLNLEFGGFPKGHGLPQEGVLSRVLMIYLDRFDHEFYRISMRHEALGLDS

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VRLPALQKEEAMFLGTVIIGKKNLGHGLKKVKBSEIKGLADSNSTLSQLSCHRKARAK

TDHWKKILLRINMEDVLRTSADRSEEFYLSKHVEPTVPQELENAFYKEQNAAAAYVS

SETANLEALLPCPQSHDRPVFFGDVVAPTNAIGRKRFKYKGLITAKGYARSNSMILLLD

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TDLELSTIPSAABDIEQDFQHEKLDSPAPDRDEHLTYGLSNSGLCLSLARLVSESSRPC

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TAQIIDWYSGLVERWYINYEGCSNFDEIKALINGIRNSGLETLAAKVRIENBEIEKR

TAQIIDWYSGLVERWYINYEGCSNFDEIKALINGIRNSGLETLSLARLVSESSRPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="POLY_A" 9791. .9912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"similar to brassinosteroid insensitive 1
GB:AAC49810 (putative receptor protein kinase); contains
Pfam profiles: pr00550 Leucine Rich Repeat (17 repeats),
pr00069 Eukaryotic protein kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         marginal_shadowexon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative receptor protein kinase"
/protein_id="AAF15908.1"
/db_xref="G1:653938"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="exon
10574. .106
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<10992. .>14231
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                                                       atttacagtatctagagctctacaaaaacaacatccaaggaactataccttccgaacttg
                                                                                                          tggatttgggaaattcaaacctctctggacatcttgcgcctgagcttgggaagcttgaac 386
                                      GTTTGAAGTTCTTGATTCTTGCTTATAATAACTTCAGTGGCGATATACCACAGGAGTATG 12162
                                                                                           TAGATTTGGGCTACAACAATTTCTCGGGACAGTTACCTACTGAAATTTCTCAGATACAGA 12102
                                                                                                                                                 172;
                                                                                                                                                            Similarity
                                                                                                                                               Conservative
                                                                                                                                                           8.2%;
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                                                                                                                                                           Score 80.8;
Pred. No. 8
                                                                                                                                               Mismatches
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AC015446/c
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Theologis, A. and Davis, R.W.
Direct Submission
Submitted (16-NOV-1999) DNA Sequencing and Technology Center, Submitted (16-NOV-1999) DNA Sequencing Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Nguyen, M., Lam, B., Southwick, A., Miranda, M., Brooks, S., Buehler, E., Chao, Q., Chin, C., Cholou, J., Chol, E., Gonzalez, A., Howng, B., Johnson-Hopson, C., Khan, S., Kim, C., Koo, T., Lee, J.M., Lenz, C., Liu, A., Liu, S., Mukharsky, N., Pham, P., Sakano, H., Shinn, P., Toriumi, M., Vaysberg, M., Yu, G., Ecker, J., Theologis, A.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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AC015446.2 GI:6692247
HTG: HTGS_PHASE1.
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Arabidopsis thaliana chromosome I clone
PROGRESS ***, 4 unordered pieces.
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                                                                                                                                                                                                                                                                                                                       n Jan 12, 2000 this sequence version replaced gi:6437511.
NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                           /organism="Arabidopsis
/db_xref="taxon:3702"
/chromosome="I"
                          /clone="F12G12"
                                                                                                                                          ocation,
                                                                                                                                                           3149: contig of 3149 bp in length
3199: gap of unknown length
12898: contig of 9699 bp in length
12948: gap of unknown length
50756: contig of 37808 bp in length
50806: gap of unknown length
112529: contig of 61723 bp in length
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  others
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** SEQUENCING
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Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H.,
Ronning,C.M., Koo,H., Fujil,C.Y., Utterback,T.R., B
Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome III BAC F18C1 genom
                                                                                                                                                                                                       Direct Submission
Submitted (18-CAN-2000) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
On Jan 18, 2000 this sequence version replaced g1:6175135.
Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                    Lin,x. and Kaul,S.
Direct Submission
Submitted (08-0CT-1999) The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Arabidopsis thaliana
                 Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ft from arthur.epm.ornl.gov), Genefinder (Phil Green, University
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                                                                                                                  The orientation of the
                                                                                                                                        BAC clone F18C1 is from Arabidopsis chromosome III and is near the molecular marker mi172.
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  Washington),
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  Genscan (Chris Burge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.2<del>8</del>;
53.9<del>8</del>;
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Pred. No. 1.3e-09;
0; Mismatches 140;
                                                                                                                  sequence is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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e, MD 20850, USA, xline
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PLN 18-JAN-2000 F18C1 genomic sequence,

86385

86505 506 86565

SP6 to T7 end of the BAC

v of

nomic Research, xlin@tigr.org

genomic sequence

., Haas,B., Wu,D Barnstead,M.E.,

Wu, D.,

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FEATURES
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                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
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Incation/Qualifiers

Inceation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:AAC27644"

join(15397. 15585,16169. 16247,16449. 16543,16641. 16772,
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18413. 18540,18736. 19141)
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18413...18540,18736...>19141)
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ement(14500
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24593. .>24701)
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δÃ ₽ Ş Š 닭 Ş ઠ Ω 밁 밁 Š Query Match 8.1%; Score 79.8; DB 50; Best Local Similarity 53.3%; Pred. No. 1.4e-09; Matches 168; Conservative 0; Mismatches 147; 55747 55567 AACTTCAGTGGTTGGATTCCTTCTTCCCTTGGAAACCTTTTTCACCTCACCTCTCCCAC 55626 55867 ACGCTTCCTCCTAAC 55881 524 ttgaagtctctggtctttttacggcttaatgacaaccgattgaccggtccaatccctaga 583 344 aacctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatctagag 403 acaatcccaacaaac 658 TTGAACCAATTGTCTATTTTACGTCTTGATAATAATAAGCTTAGTGGTAACCTCCCACTT 55806 Length 100887; Indels 0; Gaps 0;

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O. longistaminata
CF-5 pathogen resi
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Tomato $421 clone
Tomato $21 clone
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Rice $421 disease
Maize $421 gene DT
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Tomato RRK gene cl
Arabidopsis steroi
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O. longistaminta X
Daucus carota SERK
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20-NOV-1997.

13-MAY-1997; E02443.

R 14-MAY-1995; GB-010044.

N (NOVS) NOVARTIS AG.

I De Vries SC, Hecht VFG, Schmidt EDL, Van Holst OR WPI; 98-086529/08.

P-PSDB; W47019.

PF Production of apomictic seeds - useful in plant PF Production of apomictic seeds - useful in plant PS Claim 28; Pages 75-77; 123pp; English.

CC The sequence is that of an EST clone showing CE SERK LER (leucine-rich repeat) sequences.
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V06587:
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clone.
receptor kinase; apomixis; apomictic; seeds; produc
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
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V06585

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Minimum Maximum

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summaries

Database

N_Geneseq_36:*

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

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Scoring table:

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US-09-180-798-24 981

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V06586;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST cl
receptor kinase; apomixis; apomictic; seeds; pr
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Key
CDS
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20-N0V-1997, E02443.
13-MAY-1996; GB-010044.
[NOVS] NOVARTIS AC.
[NOVS] NOVARTIS KC.
DE VI165 SC, Hecht VFG, S
WFI; 98-08559/08.
P-PSDB; W47018.
                 production of apomictic seeds - useful in Claim 28; Pages 71-73; 123p; English. The sequence is that of an EST clone show! SERK LRR (leucine-rich repeat) sequences. Sequence 1106 Bp; 331 A; 258 C;
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KW receptor kinase; apomixis; apomictic; seeds; pr

W plant breeding; leucine-rich repeat; ss.

S Arabidopsis thaliana

Location / CDS
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Best Local s
Matches 885
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20-N0V-1997; E02443,
13-MAY-1996; GB-010044.
(NOVS) NOVARTIS AC.
(NOVS) NOVARTIS AC.
De Vries SC, Hecht VFG, $
WPI; 98-08559/08.
P-PSDB; W47022.
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The sequence is that of an EST clone showing high SERK LRR (leucine-rich repeat) sequences.
Sequence 1063 BP; 313 A; 242 C; 206 G;
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N W09743427-A1.

P 13-MAY-1997; E02443.

F 14-MAY-1996; GB-010044.

R 14-MAY-1996; GB-010044.

A (NOVS ) NOVARTIS AG.

De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

R WPI: 98-086529/08.

R P-PSDB; W47020.

P Production of apomictic seeds - useful in plant breeding Claim 28; Pages 79-80; 123pp; English.

C The sequence is that of an EST clone showing high homology to SERK LRR (leucine-rich repeat) sequences.

Sequence 788 BP; 234 A; 191 C; 156 G; 207 T;
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Best Local Similarity
Matches 757; Conserv
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V06588;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous ES receptor kinase; apomixis; apomictic; seeds plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Key
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tcaaacctctctggacatcttgcgcctgagcttgggaagcttggaacatttacagtatcta
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Matches 535; Conserv
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20-N0V-1997: E02443.
13-MAV-1996: GB-010044.
14-MAY-1996: GB-010044.
(NOVS) NOVARTIS AG.
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WPI: 98-086529/08.
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Arabidopsis thaliana SERK LRR homologous EST receptor kinase; apomixis; apomictic; seeds; plant breeding; leucine-rich repeat; ss.
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V06589;
03-AUG-1998 (first entry)
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[NOVS] NOVARTIS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the propagated hybrids and could shorten and simplify the breeding process so that selfing and proyeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
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Best Local
03-AUG-1998 (first entry)
Daucus carota SERK gene.
Teceptor kinase; apomixis; apomictic; seeds;
plant bredding; ss.
Daucus carota.
                                                                                            V06571 standard;
V06571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330
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                                                                                                                                                                                                      TCCTTCTCACTCTTCACACCCATCAGTTTTGCTAATAAC 788
                                                                                                                                                                                                                           ccctttgctcacattcctttacagaactttgagaacaac 700
                                                                                                                                                                                                                                                                              ACCCTTCAAGTGTTAGATCTATCAAATAACAGACTCTCTGGTTCAGTTCCTGACAATGGC
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                                                                                                             cDNA;
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Pred. No. 8.1e-49;
0; Mismatches 193
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                                     production; embryos;
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RESULT
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Production of spomictic seeds - useful in plant breeding
Claim 21; Pages 47-51; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase.
Claim 21; Pages 47-51; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase.
Comprising: (a) transforming plant material with a nucleotide
comprising: (a) transforming plant material with a nucleotide
comprising: (a) transforming plant material with a nucleotide
comprising: (a) transforming plant material with a nucleotide
comprising: (a) transforming plant material with a nucleotide
comprising: (a) transforming plant material with a nucleotide
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containing transformed material into plants or carpel-containing
containing transformed material into plants or carpel-containing
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containing programs. Controllable and reproducible appoints provides
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controllable and reproducible appoints provides
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controllable and reproducible as crosses with the
case that sexual plants are available as crosses with the
cappaint provides and could shorten and simplify the breeding
process so that selfing and progeny testing to produce and/or
containing the provides of true-breeding programs.

Controllable gene combination could be eliminated.

Apomixis allows plant breeders to develop cultivars with
containing the provides of the produce and forage quality and maturity.

Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;
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Best Local S
Matches 199
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                                                                                                                                                                                                                                                                                                       CTTGCGTCTCAACAACAACAGCCTCTCTGGTCCAATTCCAATGTCACTGACTAATATTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATGCTTACCTTGACAAATATGGGGGTTCTTATGACATTGGAGCTTTACAGCAATAACAT
                                                                                                                                           CTCATTTTCTTTACACCTATCAGTTTTGCCAATAATTTGAATTTATGTGGACCCGT
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Pred. No. 7.8e-19;
0; Mismatches 162;
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X23526 ID XI AC XI

X23526 standard; DNA; 5940 BP. X23526;

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Best Local Similarity
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Oryza longistaminata.
W09909151-A2.
25-FEB-1999; U14841.
17-JUL-1998; U1-910386.
(REGC) UNIV CALLFORNIA.
Hulbert SH, Richter T, Roi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-1999
O. longistami
Xa21; recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins can be used for enhancing resistance to Xanthomonas in a plant, preferably in rice or tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang G;
wpI; 99-204431/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New RRK polynucleotides and nucleic acid constructs - used for generating transgenic plants resistant to Xanthomonas Claim 1; Page 52-53; 67pp; English.
This invention describes a method for conferring disease resistance
                                                                                                                                     Daucus carota SEI receptor kinase;
                                                                                                                                                                                                                                                                                                                                                                                                     2526
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                                                                                                          plant breeding;
Daucus carota.
                                                                                                                                                                                                                                                     2706 AGTICCATCCCTICA
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longistaminta xa21 gene family member A2 DNA.

21; receptor kinase-like protein; multigene family; RRK; rice;
ant disease resistance; cassava; maize; tomato; Xanthomonas; s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165;
                                                                                                                                                                                       standard; DNA;
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                                                                                                                                                  SERK gene
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/number= 1
3851. .3979
/*tag= c
                                              /note "contains 3731. .3802
                                                                                   Location/Qualifiers 3696. .6620
                                                                       /*tag=
                                                                                                                                     apomixis;
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                                                                                                                                     apomictic;
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Pred. No.
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                                                            introns"
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                                                                                                                                     seeds;
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                                                                                                                                     production; embryos;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5940;
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 RESULT
T62124
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Claim 21; Pages 40-46; 123pp; English.

CC The sequence is that encoding SERK, a putative receptor kinase. CC It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide comprising: (a) transforming plant material with a nucleotide cell membrane renders the cell embryogenic; (b) regenerating cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing cell embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant cell breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the compositic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding programs to that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with cell specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 C.
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Best Local S
Matches 98
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De Vries SC, Hecht VFG,
WPI; 98-086529/08.
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13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
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CAGTGTTATAAGAGTGTA
                                                  ctgggatccaactcttgttaatccttgtacctggttccatgtcacctgtaaccaagacaa 312
                                                                                                        AGGCGATGCATTACACAACTTACGAACTAGCTTGCAAGATCCCAACAATGTCCTGCAGAG
                       ccgcgtcactcgtgtgga
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                                                                                                                                                          7.5%;
nilarity 71.0%;
Conservative
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/*tag= 0
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/number= 8
6197. .6339
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4430. .4528
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4284 .4357
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4124. .4211
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/number= 6
4890..4967
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5295..5803
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                         330
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                                                                                                                                                          Score 74; DB:
Pred. No. 6.6e:
0; Mismatches
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                                                                                                                                                                          .6e-11;
                                                                                                                                                            40;
                                                                                                                                                                                    Length 6695
                                                                                                                                                            Indels
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10

T62124 standard; T62124; 10-JUN-1997 (fir

(first entry)

SCCCCCCCCSTTRRAPETTTESWEET

Arabidopsis Key cds

thaliana

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DNA encoding plant morphogenesis regulatory protein - useful to yield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 17pp; Japanese.
The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to yield a plant with, e.g. short stems or altered inflorescence. The MRP acts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant.

Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-AUG-1995; 216187.
24-AUG-1995; UF-216187.
24-AUG-1995; UF-216187.
(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
(CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
WPI; 97-206629/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana plant morpho; plant; morphogenesis; regulation; inflorescence; extraneous; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTATTTGCACAGTAACAAGCTGACTGGTTCAATTCCACCTGAGCTTGGAAACATGTCAA 1044
                                                                                                                                                                                                                                                     gcaatgatttgtgtggaacaatccc
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/note= "plant morphogenesis regulatory protein"
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Location/Qualifiers
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lation; short; stem; alteration;
                                                                                                                                   ΒP
                                                         apomictic;
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Pred, No. 5.5e:
0; Mismatches
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.5e-11;
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                                                       production; embryos;
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                                                                                                                                                                                                                                       Production of apomictic seeds - useful in plant breeding
Claim 26; Pages 64-67; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase.

It may be used as part of a method of producing apomictic seeds
comprising: (a) transforming plant material with a nucleotide
sequence encoding a protein which in active form in a cell or
cell membrane renders the cell embryogenic; (b) regenerating
the transformed material into plants or carpel-containing
plant parts; and (c) expressing the sequence in the vicinity
of the embryo sac. The apomictic seeds and embryos thus produced
can be developed into plant progeny. This is useful in plant
the case that sexual plant provement and cultivar development in
the case that sexual plants are available as crosses with the
apomictic plant. Apomixis provides for true-breeding, seed
propagated hybrids and could shorten and simplify the breeding
process so that selfing and could shorten and simplify the breeding
process so that selfing and could shorten and simplify the breeding
stabilise a desirable gene combination could be eliminated.
Apomixis allows plant breeders to develop cultivars with
seed and forage quality and maturity.

Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
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Best Local :
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De Vries SC, Hecht VFG,
WPI; 98-086529/08.
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                        ctgggatccaactcttgttaatccttgttacctggttccatgtcacctgtaaccaagacaa 312
CTGGGATCCTACGCTAGTGAATCCTTGCACATGGTTCCATGTCACTTGCAACAACGAGAA
                                                                         AGGTGATGCTTTGCATACTTTGAGGGTTACTCTAGTTGATCCAAACAATGTCTTGCAGAG
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3851. .3979

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Pred. No. 1.5e-10;
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985

Matches

168;

Conservative

Query Match Best Local Similarity

7.5%; 51.7%;

RESULT
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V06585 standard; DNA; 4081 B V06585; 03-AUG-1998 (first entry) Arabidopsis thaliana SERK ge receptor kinase; apomixis; a plant breeding; ds. Arabidopsis thaliana.

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New RRK polynucleotides and nucleic acid constructs - used for generating transgenic plants resistant to Xanthomonas Claim 1; Page 48-50; 67pp; English.

This invention describes a method for conferring disease resistance i plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang G;
wpI; 99-204431/17.
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17-JUL-1998; US-910386.
13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be used for enhancing resistance to Xanthomonas in a plant, preferably rice or tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa.
WO9909151-A2.
14-APR-1996 (first entry)
Partial tomato pathogen resistance
Pathogen resisitant; Cf-2.2; tomato
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sativa Xa21 gene family member E DNA.
21; receptor kinase-like protein; multigene family;
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e 9424 BP;
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63; Conservative
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                                                                                                   cDNA; 3573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2681 A;
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Pred. No. 3
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0; Mismatches
stance gene Cf-2.2
tomato; C.fulvum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2138 C;
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3.1e-10;
hes 152;
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       Avr
                           CDNA
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    A; Avr
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       9;
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RESULT
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     HERET THE SECOND DISTRICT 
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Best Local Similarity
Matches 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon esculentum. W09531544-A2.
23-NOV-1995.
11-MAY-1995; G01075.
11-MAY-1994; GB-009394.
13-DEC-1994; W0-G02812.
31-MAR-1995; GB-006658.
07-APR-1995; GB-007332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Increasing plant pathogen resistance by induction of variegation may lead to acquired resistance to a broad range of pathogens.

Claim 9; Page 85-87; 131pp; English.

T06307 is a tomato pathogen resistance gene Cf-2.2 partial cDNA clone. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.2 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulvum. C.fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 3573 BP; 1032 A; 654 C; 664 G; 1223 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1175
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WPI; 96-010949/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leaf mould; variegation; Lycopersicon esculentum.
                                               mat_peptide
                                                                                                                                                                                                                                                                                                        Pathogen resisitant; Cf-2.1; leaf mould; variegation; ds.
                                                                                                                                                                                                                                                                                                                           Tomato pathogen resistance gene Cf-2. Pathogen resisitant; Cf-2.1; tomato;
                                                                                                                                                                                                                                                                                                                                                                                                                                    T06306
                                                                                                 signal_peptide
                                                                                                                                                                                                                                                      Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cttgggaagcttgaacatttacagtatctagagctctacaaaaacaacatccaaggaact 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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/*tag= b
/*tag=
1677.
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; Pred. No. 1.8e:
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                .l.
C.fulvum;
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Best Loc
Matches
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23.NGV-1995; G01075.
11-MAY-1995; GE-009394.
11-MAY-1994; WO-G02812.
23-DEC-1994; WO-G02812.
31-MAR-1995; GB-006558.
107-APR-1995; GB-007232.
(GA7S-) GATSBY CHARITABLE FY Hammond-Rosack RE, Jones D. WPI; 96-010949/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing plant pathogen resistance by induction of variegation amay lead to acquired resistance to a broad range of pathogens. Claim 9; Page 80-83; 131pp; English.

706306 is the tomato pathogen resistance gene Cf-2.1. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.1 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulrum. C.fulrum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 6471 Bp; 2073 A; 1106 C; 1122 G; 2170 T;
                                                                                                                                                                      X23523;
17-JUN-1999 (first entry)
O. longistaminata Xa21 gene family member al DNA.
Xa21; receptor kinase-like protein; multigene family;
Xa21; receptor esistance; cassava; maize; tomato; Xant
P-PSDB; W93596.
New RRK polynucleotides and nucleic acid constructs -
generating transgenic plants resistant to Xanthomonas
Claim 1; Page 37-39; 67pp; English.
                                                                                                                                                           Xa21; receptor kinase-like plant disease resistance; Oryza longistaminata. W09909151-A2.
                                                               Wang
WPI;
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                                                                                          Hulbert SH, Richter
                                                                                                        17-JUL-1998; U14841.
17-JUL-1998; US-910386.
13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                               X23523 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        491
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99-204431/17.
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                                                                                                                                                                                                                                                                                                                                                                                                             ATTCCTGCTTCATTGGGGAATCTGAACAACTTGTCTATGTTGTATCTTTACAATAATCAG
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52.9%;
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                                                                                          Ronald
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DA, Jones
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Pred. No. 2.3e-
0; Mismatches
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                                                                                         Song W,
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.3e-09;
                                                                                          Szabo
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Best Local Similarity 51.0
Matches 160; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins on the used for enhancing resistance to Xanthomonas in a plant, preferably rice or tomato.

Sequence 8416 BP; 2220 A; 1984 C; 1707 G; 2505 T;
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                                                         TCATCCCTGGGCAAGCTCACCGGCCTCTATAATCTTGCACTGGCTGAAAATATGCTGTCT
                                                                          agagcactcacggcaatcccaagccttaaagttgttgacgtctcaagcaatgatttgtgt
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Pred. No. 4.3e-09;
0; Mismatches 154;
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Search completed: June 23, 2000, 22:53:01 Job time: 40577 sec

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Match
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465.028 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/6COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-587-680A-1
US-08-587-680A-2
US-08-587-680A-2
US-08-587-680A-2
US-08-587-680A-2
US-08-666-271-1
US-08-666-271-1
US-08-666-271-1
US-08-666-271-1
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US-08-68-292-936B-20
US-08-189-256A-16
US-08-189-256A-16
US-08-189-256A-11
US-08-724-394A-20
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US-08-567-375-3
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      TELERAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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No. 5340934	Patent No		1593		33	43	
_	Sequence	6 PCT-US95-08542-1	1026		33	42	
nce 1, Ap	Sequence	B0-SD	1026		33	41	
nce 1, Ap	Sequence		1026		33	40	
nce 26, A	Sequence	2 US-08-442-063A-26	1002		33	39	
nce 47, A	Sequence	2 US-08-442-063A-47	924		33	38	
nce 44, A	Sequence	2 US-08-442-063A-44	849	3.4	33	37	
41,	Sequence	2 US-08-442-063A-41	711		33	36	
nce 38, Appl	Sequence	2 US-08-442-063A-38	567		33	35	
35,	Sequence		426		33	34	
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nce 1, Appl	Sequence	3 US-08-508-786-1	2010	3.4	33.8	28	Q

ALIGNMENTS

Sequence 3, Application US/08567375 Patent No. 5952485 SOFTMARE: PATENTIN Release #1.0, Version #1. CORRENT APPLICATION NUMBER: US/08/567,375 #ILING DATE: 04-DEC-1995 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/004,645 FILING DATE: 29-SEP-1995 PRIOR APPLICATION PATA: APPLICATION NUMBER: US 08/475,891 #ILING DATE: 07-JUN-1995 PRIOR APPLICATION NUMBER: US 08/475,891 #ILING DATE: 07-JUN-1995 PRIOR APPLICATION NUMBER: US 08/373,375 #ILING DATE: 17-JAN-1995 APPLICATION NUMBER: US 08/373,375 #ILING DATE: 17-JAN-1995 ATTORNEY/AGENT INFORMATION: NAME: BASTLAN, KEVIN L. GENERAL INFORMATION: APPLICANT: Ronald ZIP: 94111-3834 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STREET: TWO CITY: San Francisco CTATE: California REGISTRATION NUMBER: 34,774 REFERENCE/DOCKET NUMBER: 02 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 TELEPAX: (415) 576-0300 TITLE OF INVENTION: Procedures and Materials for TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 16 COUNTRY: USA ZIP: 94111-3834 Wang, Guo-Liang Sorg, Wen-Yuang Szabo, Veronique Ronald, Pamela C. ω •• 023070-058930 Conferring

MOLECULE TYPE: FEATURE:

DNA

(genomic)

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Best Local Similarity 49.9
Matches 169; Conservative
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                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION DATA:
APPLICATION DATA:
US/08/587,680A
FILING DATE: 17-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION US/08/587,375
FILING DATE: 17-JAN-1995
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APPLICANT:
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TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1459 CCAATACCCAGTGAATTATTCAATATTCAAACACTATCA 1497
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                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 07-JUN-1995
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LOCATION:
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OTHER INFORMATION: /product= "Xa-21"
                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94111-3834
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APPLICATION DATA:
LICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Townsend and Townsend and Crew LLP
T: Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                     California
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Song, Wen-Yuang
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us 60/004,645
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Pred. No. 4.7e-10;
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; NAME/KEY: CDS
; LOCATION: Join(1..2676, 3520..3918)
; OTHER INFORMATION: /product= "Xa-21"
US-08-587-680A-3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3921 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08475891A Patent No. 5859339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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ATTORNEY/AGENT INFORMATION:
                                                                                        APPLICANT: Wang Guo-Liang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1159 AAGATCACAGGAAGCATTCCGAAGGATATTGGCAATCTTATTGGCTTACAACATCTCTAT 1218
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COMPUTER READABLE FORM
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Local Similarity 49.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                   COUNTRY:
                                                                             CITY: San Francisco
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COTHER INFORMATION: Join (512.)
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US-08-238-163-3
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                            Sequence 3, Application US/08238163 Patent No. 5569830
                GENERAL INFORMATION:
APPLICANT: BENNET
APPLICANT: LABAVI
APPLICANT: POWELL
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APPLICATION DATA:

APPLICATION NUMBER: US/08/475,891A
FILING DATE: 06-JUN-1995

CLASSIFICATION: 800

PRIOR ADDRESS: 06-JUN-1995
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APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (415) 576-0300
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REGISTRATION NUMBER: 34,774
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OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: II
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                                                                                                                                                                                                                  CCAATACCCAGTGAATTATTCAATATTCAAACACTATCA 2008
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                                 BENNETT, Alan
LABAVITCH, John M.
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POWELL, Ann
STOTZ, Henrik
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RMATION: /product= "RKF-B"
RMATION: /note= "Xa21 Xanthomonas spp. disease
RMATION: resistance gene RRK-B from rice (Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
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Pred. No. 5.8e-10;
0; Mismatches 170;
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.1%;
Best Local Similarity 49.0%;
Matches 221; Conservative
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APPLICATION NUMBER: US/08/
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94105-1493
COMPUTER READABLE FORM:
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34.774
REFERENCE/DOKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
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                                                 324 gtgtggatttgggaaattcaaacctctctggacatcttgcgcctgagcttgggaagcttg 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM FC COMPUTER: COMPUTER: IBM FC COMPUTER: PC-DOS/MS-DOS

COPTWARE: Patentin Release #1.0, Version #1.25
                  621
                                                                                                                        608
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                                                                                                                                                                                                                                                                689 CATATCTCGAAACATTGGAATTTCATCATGTTACTAATCTCACCGGAACAATTCCACCTG
                                                                                                                                                                                                                                                                                                384 aacatttacagtatctagagctctacaa---aaacaacatccaaggaactataccttccg 440
                                                                                                                                                                                                                                                                                                                                                                                                           573 AGATTGCTGTTACTGGTACGTCATAAAATGTGACCGGAAAAC----CAACCGGATAAATG 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Stewn Francisco
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totcaagcaatgatttgtgtggaacaatccc 651
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                                                                                                                                                                                            CAATTGCGAAGCTCACAAATCTCAAAATGTTAAGGCTCAGCTTCACTAACCTTACAGGTC
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                                                                                                                        CGATCCCTGAATTCCTTAGTCAGCTGAAGAATTTGACGTTGCTCGAGTTGAATTACAATC
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Pred. No. 3.3e-08;
0; Mismatches 223;
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                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 168; Conserv
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Guo-Liang APPLICANT: Song, Wen-Yuang
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
2855
                                                                        2795
                                                                                                                                                  2735 TGGACTTGGGAGAAAATAACCTGGGGGGGAGTTCTTCCTAATTCGTTTTCCAATCTTTCCA 2794
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OTHER INFORMATION:
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STATE: Calter
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/475,891A FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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LOCATION: joir
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                  ttggaaatctgaagaatctcatcagcttggatctgtacaacaaccatcttacagggatag 503
                                                                                              att---tacagtatotagagototacaaaaacaacatocaaggaactatacottocgaac 443
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                                                                          CTTCGCTTAGTTTTCTTGCACTTGATTTGAATAAGATCACAGGAAGCATTCCAAAGGATA 2854
TTGGCAATCTTATTGGCTTACAACATCTCTATCTCTGCAACAACAATTTCAGAGGGTCAC 2914
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                                                                                                                                                                                                                                               6.1%;
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/note= "xa21 xanthomonas spp. disease resistance gene RRK-F from rice (Oryza sativa)"
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Pred. No. 5.6e-08;
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US-08-567-375-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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APPLICATION NUMBER: US 0:
FILING DATE: 07-JUN-1995
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PRIOR APPLICATION DATA:
APPLICATION UNMER: US 60/004,645
FILING DATE: 29-SEP-1995
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CURRENT APPLICATION DATA:
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                                                                                                                                   FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CITY: San Francisco
                                                                                                                                                                                     LENGTH: 6256 base pairs TYPE: nucleic acid STRANDEDNESS: single
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                                 INFORMATION:
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Song, Wen-Yuang
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                                                     join(1648..4383, 5178..5513)
WATTON: /product= "RRK-F"
WATTON: /note= "Xa21 Xanthomonas spp. disease
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                                                                                                                                                   DNA (genomic)
                   resistance gene RRK-F from (Oryza sativa)"
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GENERAL INFORMATION:
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Best Local
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP
ADDRESSEE: Townsend and Townsend and Crew LLP
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                                                                                                                                                                             APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION NDATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/01
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27
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Local Similarity 51.18;
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NAME: Bastian, Kevi
REGISTRATION NUMBER:
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Song, Wen-Yuang
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34,774
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Pred. No. 5.6e-08;
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RESULT 8
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APPLICANT: BENNETT
APPLICANT: LABAVII
APPLICANT: POWELL,
APPLICANT: STOTZ,
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08238163 Patent No. 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 023U
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
""" FFAX: (415) 576-0300
""" FFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
        ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2975
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                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                               TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE
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LOCATION: join(1648...4383, 5178...5513)
OTHER INFORMATION: /product= "RRK-F"
OTHER INFORMATION: /note= "xa21 xantho
OTHER INFORMATION: resistance gene RRK
OTHER INFORMATION: sativa)"
                                                                                             COUNTRY:
                                                                                                                                     CITY:
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OPERATING SYSTEM:
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                                                                                                                                     San Francisco
                                                                                                                California
                                                                                                                                                                                                                                                                                                            LABAVITCH, John
                                                                                                                                                                                                                                                                                                                               BENNETT, Alan
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STOTZ, Henrik
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PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "RRK-F" disease /note= "%a21 Xanthomonas spp. disease resistance gene RRK-F from rice (Oryza sativa)"
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Pred. No. 5.6e-08;
); Mismatches 158;
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

US/08/238,163

Floppy disk

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RESULT 9
US-08-473-553A-1
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; OTHER INFORMATION: /standard_name= "Pear PGIP cDNA"
US-08-238-163-1
                                                                                                                                                                                                                                                          Sequence 1, Application US/08473553A Patent No. 5859338 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.8%;
Best Local Similarity 52.0%;
Matches 127; Conservative
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BASTLAN, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach,
STREET: Four Embarcadero Co
                                                                                                                                            APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 03-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 1..1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aattgaagtctctggtctttttacggcttaatgacaaccgattgaccggtccaatcccta 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCACATTCCTCGACCTCTCCTTCAACAACCTCACCGGTGCCATCCCCAGCTCGCTTTCTG
               RY: United States
94111-4187
                                                   San Francisco
: California
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34..1023
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Pred. No. 2.3e-07;
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                                                                                        Albritton & Herbert
Suite 3400
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                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: A-60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.6%;
Best Local Similarity 51.0%;
Matches 129; Conservative
                                                                                                                                                                                                                                   Sequence 24, Application US/08587680A Patent No. 5977434
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APPLICATION NUMBER: US/CELING DATE: 06-JUN-1999
CLASSIFICATION: 800
                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
FEATURE:
                                                                   APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Scabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                         3180 GATCCTCGACATGGCGAGCTGTACACTCACCGGAGAGATTCCGACGAGTTTAAGTAACCT 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3120 CTACTACAACAGCTACACCGGTGGTGTTCCACGCGAGTTCGGTGGTTTAACAAAGCTTGA 3179
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NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,
              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLF
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                           3360 AATCCCTCAAAGC 3372
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COMPUTER: IE
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San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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5117..5467
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2434..5037
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Pred. No. 2.3e-06;
0; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5733;
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COUNTRY:

STATE: California

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RESULT 11
US-08-567-375-15
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ATTORREY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058940US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1876-0200
                                   Sequence 15, Applicat Patent No. 5952485
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.5%;
Best Local Similarity 49.1%;
Matches 143; Conservative
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 29-SEP-195
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDN
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     466 cagcttggatctgtacaacaaccatcttacagggatagttcccacttctttgggaaaatt 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 cctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatctagagct 405
                                                                                                                                                                                                                                                           198
                                                                                                                                                                                                                                                                              526 gaagtetetggtetttttaeggettaatgaeeagetgaetggaeeggteeaateeetagage 585
                                                                                                                                                                               258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1554 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 17-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 CTTGTCTGGTGCACTTCCTAGTGCTATTGGAAACTATTCAGGGCTGAAGAATCTTGTGTT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                           ctacaaaaacaacatccaaggaactataccttccgaacttggaaaatctgaagaatctcat 465
                                                                                                                                                                                                               actcacggcaatcccaagccttaaagttgttgacgtctcaagcaatgattt 636
                                                                                                                                                                                                                                                         TCTTTCCTTAACTTACTTGGATTTGAGCCAAAATCAACTTTCTGGTCCTATCCCAGTTCA
                                                                                                                                                                                                                                                                                                                                     AAAGCTGGACCTGAGTAGAAACAACTTCTCTGGCACAATCCCTCCTCAGATTGGTAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                 AACTGGAAATGGTTTCTCAGGTGATATCCCTTCTGATATTGGCAGACTAAAGAGCATCTT 137
                                                                                                                                                                               AATTGCTCAAATTCACATCTTAAATTACATCAATATTTCCTGGAATCACTT 308
                                                                            Application
Wang, Guo-Liang
                Ronald, Pamela C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA (partial)
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                                                                         us/08567375
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Pred, No. 1.6e-06;
0; Mismatches 148;
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: D
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COMPUTER: COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION: 800
PION APPLICATION DATA:
APPLICATION UNMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PION APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/475,891
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNET/AGENT INFORMATION:
NAME: BASTIST INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
                                                                                                                                                                                                                                                                                                                                                                         351 ctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatctagagctctaca 410
                                                                                                                                                                                                                                                                                  411 aaaacaacatccaaggaactataccttccgaacttggaaatctgaagaatctcatcagct 470
                                                                                  213
                                                                                                                   531 ctctggtctttttacggcttaatgacaaccgattgaccggtccaatccctagagcactca 590
                                                                                                                                                                     153
                                                                                                                                                                                                               471
273 CTCAAATTCACATCTTAAATTACATCAATATTTCCTGGAATCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                        93 GANATGGTTTCTCAGGTGATATCCCTTCTGATATTGGCAGACTAAAGAGCATCTTAAAGC 152
                                                                                                                                                                                                                                                                                                                                           33 CTGGTGCACTTCCTAGTGCTTTTGGAAACTATTCAGGGCTGAAGAATCTTGTGTTAACTG 92
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                                  cggcaatcccaagccttaaagttgttgacgtctcaagcaatgattt 636
                                                                                CCTTAACTTACTTGGATTTGAGCCAAAATCAACTTTCTGGTCCTATCCCAGTTCAAATTG
                                                                                                                                                                     TGGACTCGAGTAGAAACAACTTCTCTGGCACAATCCCTCCTCAGATTGGTAACTGTCTTT
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California
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Szabo, Veronique
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ilarity 48.3%;
Conservative
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3.3e-05;
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318
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Best Local Similarity 48.5%;
Matches 133; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: Sincl
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: GB 9. FILING DATE: 11-MAY-1994 ATTORNEY/AGENT INFORMATION: NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: GB 9: FILING DATE: 24-DEC-1993 PRIOR APPLICATION DATA:
                                                             2193
                                                                                                                               2133
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PRIOR APPLICATION DATA:
PCT/GB94/02812
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517
                                                                                                                                                                                               2073 TATCAATCTCTCAAAGAACAGATTTGAAGGTCATATTCCAAGCATTATTGGAGATCTTGT 2132
                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                 577 ccctagagcactcacggcaatccccaagccttaaagttgttgacgtctcaagcaattgattt 636
                                                                                                                                                              457
                                                                                                                                                                                                                  397 totagagototacaaaacaacatocaaggaactatacottocgaactttggaaatotgaa 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
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                                                                                       gggaaaattgaagtotctggtotttttacggcttaatgacaaccgattgaccggtocaat 576
                                                                                                                                                         gaatctcatcagcttggatctgtacaacaacaatcttacagggatagttcccacttcttt
                                                                                                                               TGGACTTCGTACGTTGAACTTGTCTCACAATGTCTTGGAAGGTCATATACCGGCATCATT 2192
                                                             TCAAAATTTATCAGTACTCGAATCTTTGGATCTCTCATCTAATAAAATCAGCGGAGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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THOMAS, COLWYN M
JONES, DAVID A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703-816-4100
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11-MAY-1994
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                                                                                                                                                                                                                                                             141; Indels
                                                                                                                                                                                                                                                                                             Length 2880;
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2312
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US-08-666-271-1
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Query Match
Best Local Similarity
Matches 133; Conserv
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                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 3905 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 11-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 23-DEC-1994 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                        NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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THOMAS, COLWYN M
JONES, DAVID A
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JONES, JONATHAN D
JONES, JONATHAN D
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                48.5%;
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Score 48.4; DB 4;
Pred. No. 0.00012;
0; Mismatches 141
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                              Length 3905;
   Indels
   0;
   Gaps
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US-08-232-463-14
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US-08-232-463-14
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14,
                                 Query Match
                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/935
APPLICATION NUMBER: US/07/935
FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY_AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 39,768
REFERENCE_POCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                           TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DORNER, F.

APPLICANT: SCHEIFLINGER, F.

APPLICANT: FALKNER, F.G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rel-base #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3093
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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   Local Similarity
hes 12; Conserva
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4.8%; Score 47.4; DB 1; llarity 3.5%; Pred. No. 0.00032; Conservative 194; Mismatches 135;
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                                 Length 7218;
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INFORMATION FOR SEQ ID NO: 1-
SEQUENCE CHARACTERISTICS:
SEQUENCE 1116 base pairs
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APPLICANT: Cervon
                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: IT RM 91A
FILING DATE: 06-DEC-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/IT
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: SULLIVAN, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 19-9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Sally A. Sullivan
STREET: 5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compa
OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleotide Sequences Coding An TITLE OF INVENTION: Endopolygalacturonase Inhibitor NUMBER OF SEQUENCES: 17
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                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                 TELEPHONE:
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                                                                (303)499-8080
(303)499-8089
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Salvi, Giovanni
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                            JMBER: US/08/244,646
06-JUN-1994
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                                                                                                                                                                                                       WO PCT/IT/00158
                                                                                                                                                                                                                                                          IT RM 91A 000915
                                                                                                                      19-94
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FEATURE:
NAME/KEY:
LOCATION:
US-08-244-646-14
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Search completed: June 23, 2000, 22:45:22 Job time: 40268 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI - SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phaseolus vulgaris
STRAIN: Saxa
IMMEDIATE SOURCE:
CLONE: lambda PGIP-3.3
                                                                                                                                                              582 CCC 584
                                                                                                             522 CTCTTCTCCCCCAACCTCGGAGGAATCACATTCGACGGCAACCGAATCTCCGGCGCCCAT 581
                                                                                                                                589 cacggcaatcccaagccttaaagttgttgacgtctcaagcaatgatttgtgtggaacaat 648
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LOCATION: 1..1026
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Listing first 45
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              4857316 seqs, 2026611650 residues
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(without alignments)
641.482 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 3 3 A1992868 469 bp mRNA EST 08-SEP-1999 1701493826 A. thallana, Ohio State clone set Arabidopsis thallana CDNA clone 701493826, mRNA sequence. A1992868 A1992868.1 GI:5839773 S EST. Ism Arabidopsis thallana Examination viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. I (bases to 469) Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D., Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P., Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D., Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C., Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobriga,A., Murry,L., Turner,C., Krikorlan,S., Elder,L. and	ALIGNMENTS	512 64 AW036955 541 64 AW040482 304 36 T21150 568 47 AI487772 423 35 C22371 570 50 AI67639 510 64 AW033599 258 42 AI100678	26.6 26.1 26.1 25.9 25.9 25.9 24.6 24.6 24.6 24.6 24.6 24.6 24.6 24.6	31.1 337 20 234606 31.1 337 20 234606 30.4 339 42 ANILO0679 29.8 667 80 AW250720 29.8 657 80 AW250720 29.7 336 23 H37296 29.4 511 74 AW2211278 29.2 714 64 AW031188 29.8 234 23 H37195 27.8 695 64 AW038168 27.8 695 64 AW038168	41.1 469 63 A1992868 39.2 556 23 R89998 36.7 534 33 AA394359 36.0 447 23 H36800 35.0 401 37 AA712221 34.2 353 23 H37300 34.2 353 23 H37300 33.9 364 42 A1100683 33.9 364 42 A1100683 33.5 336 20 Z34187 32.2 348 42 A1100682 31.9 608 81 AW443205	Score Match Length DB ID Description
Qy 417 acatccaaggaactataccttccgaacttggaatctgaagaatctcatcagcttggatc 476	Db 343 ATCTTGCGCCTGAGCTTGGGAAGCTTGAACATTTACAGTATCTAGAGCTCTACAATAACA 402	Qy 237 accatgtcctccagagctgggatccaactcttgttaatccttgtacctggttccatgtca [Onigin Autority Matches 412; Conser	TITLE Arabidops JOURNAL Unpublish COMMENT On Dec 20 Contact: Genome Sy Pharmaceu 4633 Worl Tel: 877- Fax: 314 Email: se	Hanson, D.

RESULT 1
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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                                                    ttgg-agggaccggaattactcggtcttgcaagctacgacactaactgcacctgaaacaa 765
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MSU-DOE Plant Research Laboratory
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| primer: T7 dye primer.
| cocation/Qualifiers
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/clone="187H5T7"
/clone_11b="Lambda-PRL2"
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/strain="var columbia"
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92.9%;
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CACTCACGGCAATCCCAAGCCTTAAAGTTGTTGACGTCTCAAGCAATGATTTGTGTGGAA
                                                                                                                                      TGAAGCCTCTGGTCTTTTTACGGCTTAATGACAACCGATTGACCGGTCCAATCCCTAGAG
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1 (bases 1 to 534)

1 (bases 1 to 534)

Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,

McIntosh, L., Ohlrogge, J., Respectively.

McIntosh, L., Charles, M., Seeder, J., Respectively.

McIntosh, L., Charles, M., McIntosh, 
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Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
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euphyllophytes; Spermatophyta; Magnoliophyta;
eudicots; Rosidae; eurosids II; Brassicales; 1
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114 c 125 g 126 t 18 others
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/strain="var columbia"
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Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
Michigan State University, Plant Biology
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14929 Lambda-PRL2 Arabidopsis thaliana
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Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Ralkhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
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Tel: 517-353-0854
Fax: 517-353-9168
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                                /clone_lib="Lambda-PRL2"
//note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox equal
quantitles of 4 pools of mRNA. The mRNA sources were 1) /
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
saliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA."
              oligo dT primed cDNA.
115 c 83 g
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/clone="179A22T7"
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/strain="var columbia"
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AA712221.1
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Tel: 517-353-0854
Fax: 517-353-9168
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                                                                                                                                               il: 22313tcn@ibm.cl.msu.edu
primer: T7 dye primer.
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Lambda-PRL2
/organism="Arabidopsis thi
/strain="var columbia"
'/db_xref="taxon:3702"
/clone="18009T7"
/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip
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Raikhel,N., Somerville,
Zip-Lox;
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,S., Thomashow, M.,
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                                                                                                                                                                                                                                                                                             sequence.
H37300
H37300.1 GI:
EST.
thale cress.
95148729
On May 8, 1995 this sequence versi
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State Univer
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15429 I
                                                                                                  Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashov Retzel,E. and Somerville,C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA (Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                           Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Lambda-PRL2
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        University, Plant
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Tel: 517-3
Fax: 517-3
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                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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1 (bases 1 to 364)
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Seq primer: T7 dye primer.
              Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thom
                                                                                                                                    Arabidopsis thaliana
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//clone_lib="Lambda-PRL2"
//clone_"Vector: lambda Zij-Lox; Site_l: Sal; Site_2: Not;
//clone_"Vector: lambda Zij-Lox; Site_l: Sal; Site_2: Not;
//clone_lib="Lambda-PRL2"
//clone_"Vector: lambda Zij-Lox; Site_l: Not;
//clone_"Vector: lambda Zij-Lox; Not;
//clone_"Vector: lambda Zij-Lox; Not;
//clone_"Vector: lambda Zij-Lox; Not;
//clone_"Vector: lambda Zij-Lox; The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. "

98 a 85 c 67 g 89 t 14 others
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/strain="var columbia"
and
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Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ib
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The sequence entry for this EST
is being submitted in the sense
Seg primer: M13-21.
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//note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
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/strain="var columbia"
/db_xref="taxon:3702"
/clone="187H5XP"
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AI100682 348 33803 Lambda-PRL2

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EST cDNA clone

21-AUG-1998 185L1XP 3',

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                                                                                          acaaaaaaaatgaagaatcgaatcggtaatatcatctggtctcaattgagaacttcgagg
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TCTGTATGTAAAATTTCTAAAGTCGATTTTCGC
                                                                        ACAAAAAATGAAGAATCGAATCGGTAATATCATCTGGTCTCAATTGAGAACTTCGAGG
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Z34187.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratoire de Biologie Cellulaire
Route de Saint-Cyr, 78026 Versailles
Email: thierry@versailles.inra.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Arabidopsis thaliana transcribed genome: Unpublished (1996)
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/strain="ecotype Columbia"
/db_xref="taxon:3702"
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/clone_1ib="Versailles-VB"
/clsue_type="whole seedlings"
/tissue_type="whole seedlings"
/dev_stage="in vitro-grown etiolated seedlings,5
/note="Vector: pBluescript"
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Pred. No. 4.8e-73;
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                                                                                                                                                                      CCGGBATTACTCGGTCTTGCAAGCTACGACCTGAACCTGGACACACTGGCACACAC 775
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                         CTGAAAATGAAGAATTGGGGGGTGANCTTGTAAGAACACTTCACCACTTTATCAAATATC
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     ACATCTACTATGTAATAAGTATATATGTAGT 346
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Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
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Newman,T., deBruijn,F.J., Green,P., K.
McIntosh,L., Ohlrogge,J., Raikhel,N.,
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Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
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Tel: 517-353-0854
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The sequence entry for this EST
is being submitted in the sense
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/strain="var columbia"
/db_xref="taxon:3702"
/clone="185L1XP"
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., Somerville,S., Thomashow,M.,
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                                                              actcgtgtggatttgggaaattcaaacctctctggacatcttgcgcctgagcttgggaag
                                                                                                           CCAAATCTTGTTAACCCTTGTACCTGGTTTCATGTCACTTGCAACGGAGATAATCAAGTT
                                                                                                                               ccaactcttgttaatccttgttacctggttccatgtcacctgtaaccaagacaaccgcgtc
                                                                                                                                                                                  GCTTTGTACGCCCTCCGCGGGAGCTTATCTGACCCGGGTAACGTGTTACAGAGCTGGGAT
                                                                                                                                                                                                                                                          GGTTTGTTGGCAGTTGTTCTTGCTGTAGCTGTGGCTGTAAAAGGGGAATTCAGAAGGGGAT
cttgaacatttacagtatctagagctctacaaaaacaacatccaaggaactataccttcc
                                   ACTCGTGTGGATCTTGGGAACTCAAAGTTATCTGGTCATTTGGTACCTGAGCTCGGAAAG
                                                                                                                                                                                                                                                                                                                                   411;
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100 Jordan Hall, Cl
Tel: 864 656 4366
Fax: 864 656 4293
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Eukaryota; Viridiplanta
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Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
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                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                 Score 312.6; DB 8
Pred. No. 6.2e-69;
0; Mismatches 164
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Indels

0;

Gaps

0

92 199

212

319 152

379

439

D'Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Liang, F., Hansen, T.S., Ronning, C.M., Craven, M.B., Bowne Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; On Dec 20, 1995 this sequence version replaced gi:1135853 Generation of ESTs from tomato callus (mixed elicitor) /note-"vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; CLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning." /clone_lib="tomato mixed elicitor, /tlssue_type="leaf" /dev_stage="4-5 week old plants" /lab_host="xil-Blue MRF'" /organism="Lycopersicon esculentum" /cultivar="Rio Grande PtoR" /db_xref="taxon:4081" BTI Lycopersicon esculentum cDNA DB 81; Length Bowman, C 17-FEB-2000 608; Holt, I.E.,

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SOURCE
ORGANISM
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BASE COUNT
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EST274417
CLEC13C21
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1 (bases 1 to 720)

1 (bases 1 to 720)

Alcala,J., Vebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                        100 Jordan Hall, Clemson,
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute Clemson University
                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
On Dec 20, 1995 this sequence
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
AW031110
AW031110.1 GI:5889866
                                                                                                                                                                                                                                                                                                                                                                                     Generation of ESTs from tomato callus tissue
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               200
                                                                                                                                                                                                                                                            dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                 sequence.
               þ
            /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; supplier: Giovannoni laboratory; cLEC - cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library" a 149 c 143 g 228 t
                                                                                                                           /clone="clEC13021
/clone_lib="tomato callus,
/tissue_type="callus"
/tissue_type="callus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      720 bp mRNA EST 15-SEP-1999 tomato callus, TAMU Lycopersicon esculentum cDNA c. similar to leucine-rich repeat protein (LRR), mRNA
                                                                                                           /dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                             /cultivar="TA496"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                          organism="Lycopersicon"
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                                                                                                                                                                                                                                                                                                                                                         version
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Best Local S
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
Z34606
Z34606.1 GI:507009
                                                                                                                                                                                                                                                                                                                                                                                                               Z34606 337 bp
ATTS3366 Versailles-VB
                             Laboratoire de Biologie Cellulaire
Route de Saint-Cyr,78026 Versailles
Email: thierry@versailles.inra.fr.
                                                                                                                           The Arabidopsis thaliana transcribed genome:
Unpublished (1996)
Contact: Desprez T., Amselem J., Chiapello H
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Location/Qualifiers
1. .337
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Pred. No. 1.1e-68;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
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                                                                                                                                   Rouze
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                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                  Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
                                                                                  On May 5, 1995 this sequence version replaced Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DE-PKL, Michigan State University, Plant
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33800 Lambda-PRL2
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22313tcn@ibm.cl.msu.edu quence entry for this EST
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/strain="ecotype Columbia"
/db_xref="taxon:3702"
/clone="VBVDH02"
/clone_lib="Versailles-VB"
/tissue_type="whole seedlings"
/tissue_type="whole seedlings"
/dev_stage="in vitro-grown etiolated seedlings,5 /
/dev_stage="in vitro-grown etiolated seedlings,5 /
/dev_stage="in vitro-grown etiolated seedlings,5 /
/note="Vector: pBluescript"
98 c 60 g 105 t 1 others
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Seg prime
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.

Generation of ESTs from tomato fruit tissue Unpublished (1999)
                                                                                                                                         Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                          Lycopersicon.

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Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour 119ht
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA.

75 c 66 g 89 t 5 others
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/organism="Arabidopsis
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/db_xref="taxon:3702"
/clone="179J11XP"
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Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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//note="vector: pBlueScript SK(-); Site_1: EcoRl; Site_2:
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//note="vector: pBlueScript Structure; Site_2: And the sector on the breaker (first sign of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888)919-3324 or (314) 427-3222 FAX:(888)919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome ystems.com web site:www.genomesystems.com or info@genome ystems.com web site:www.genomesystems.com
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Fax: (217) 333-4582
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                                                                                                                                                                                                                University of Illinois,
http://www.life.uiuc.edu/biotech/keck.html."
131 c 120 g 191 t 25 others
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Search completed: June 23, 2000, 19:06:35 Job time: 27428 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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De, V.S., Schmidt, E.D., Van, H.G. and Hecht, V.F.
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De, V.S., Schmidt, E.D., Van, H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;
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1 (bases 1 to 1106)
De, V.S., Schmidt, E.D
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DHYLQSWDPTLYNPCTWFHYTCNQDNRYTRYDLGNSNLSGHLAPELGKLEHLQYLELY
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                                         TGATTATCTGAAAACATTTACATTATCAGTCACACATATAACATTTTGCTTTGAGTCATA
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1 (bases 1 to 894)

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De, V.S., Schmidt, E.D., Van, H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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NVLQSWDPTLVWPCTWFPHYCNNENSVIRVDLGANELSGHLVPELGVLKNLQYLELYS
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Hipskind, J.D., Nicholson, R.L. and Goldsbrough, P.B.
Isolation of a cDNA encoding a novel leucine-rich
Sorghum bicolor inoculated with fungi
MOL Plant Microbe Interact. 9 (9), 819-825 (1996)
97124217
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                                                                                                                     Direct Submission
Submitted (26-JUN-1996) John D. Hipskind, Bot
Pathology, Purdue University, West Lafayette,
                                                                                                                                                                                                                                                                                                                                                                                                   викатуота; Viridiplantae; Streptophyta; Embryophyta; Tracieuphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poaceae; Sorghum.
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/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone="SLRR"
12. .755
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U93048
U93048.1 GI:2
1 (bases 1 to 1755)
Schmidt, E. D., Guzzo, F., Toonen, M.A. and de Vrie
A leucine-rich repeat containing receptor-like
plant cells competent to form embryos
Development 124 (10), 2049-2062 (1997)
                                                                                      Daucus carota
Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
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/db_xref="GI:1710124"
/translation="MAPOPAAAGFLITGLLALATFASCNTEGDILYKQRLAWEDPNNVL
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OSNNSTLANFCTWFHYTCINNNWFVIRVDLGNAGISGFLLPDLAEIQNLQYIELYGNGL
NGSIPETLGNLTNLISLDLWDNLLTGEIPTLGSYSTLRYLRIYQNNLTGPIPSSFGN
LTSLLESKLQENSLSGAIFASLGNIKALOFSRLNDNMLTGTVPSKSFFLSTFGNLTEL
NTDRNNLDGTRTSSGLRVTAIIQDALKTA"
36. 77
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/note="leucine-rich repeat-containing extracellular
glycoprotein; contains six N-glycosylation sites
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embryogenesis
                                                      Toonen, M.A. and de Vries,
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No. 8.2e-34;
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2 (bases
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Location/Qualifiers
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Submitted (12-MAR-1997) Molecular Biology, Ag
Common Provention 3, Wageningen 6703
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Schmidt, E.D.L., Guzz
Direct Submission
Eukaryota;
            Daucus
                           carrot.
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VRGTILGYIĀPĒYLSTGKSSEKTDVFGYGIMLLELITGGRĀFDLĀRLANDDVMLLDWV
KSLIKEKKLEMLVDPDLENDTĒVEQLIQVĀLLCTGGSPMERFKMSEVVRMLEGDG
LĀEKKDĒMQKVEVIHODVĒLĀPHRISEMILDSTDNLHĀFĒLSGPR*

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/product="somatic embr
/protein_id="AAB61708.
/db_xref="GI:2224911"
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2 from Patent
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/db_xref="taxon:4039"
                                                  GI:4756623
 Viridiplantae;
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Streptophyta; Embryophyta; Tracheophyta;
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1 (bases 1 to 1815)

De, V.S., Schmidt, E.D., Van, H.G. and Hecht, V.F.

PRODUCTION OF AFOMICTIC SEED

Patent: WO 974347-A 20-NOV-1997;

CIBA GEIGY AG (CH)
                                                                                                                                                                     498
                                           L.esculentum LRP gene.

X95269

X95269.1 GI:1619299

LRP gene; LRR protein.
                                                                                                  LELRPGENE
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                 tomato.
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/db_xref="taxon:4039"
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2 (bases 1 to 4604)

Tornero, P. Mayda, E., Gomez, M.D., Canas, L., Conejero, V. and Vera, P. Characterization of LRP, a leucine-rich repeat (LRR) protein from tomato plants that is processed during pathogenesis

Plant 7, 10 (2), 315-330 (1996)
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/gene="LRP"
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2709. .29
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/gene="LRP"
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/gene="LRP"
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SDPGNVLQSWDPNLVNPCTWFHVTCNGDNQVTRVDLGNSKLSGHLVPELGKLEHLQYL
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/gene="LRP"
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/gene="LRP"
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/gene-"LRP"
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/product="LRR protein"
/protein_id="CAA64565.1"
/db_xref="GI:1619300"
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/cultivar="VFN8"
/db_xref="taxon:4081"
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/gene="LRP"
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Genes were identified by a combination of three methods: Gene prediction programs including GRAII (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/EENSCANW.html), and NetplantGene (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are
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                                                                                                                                                                                                                                                                                                                                                                                                                    e-mail: xiin@tigr.org
BAC clone F9F8 is from Arabidopsis chromosome III and is near the
molecular marker g4547.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (08-OCT-1999) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
On Oct 8, 1999 this sequence version replaced g1:5902413.
Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-SEP-1999) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 101284)
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Lin.X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B.,
Lin.X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B.,
Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M
Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome III BAC F9F8 genomic sequence
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Direct Submission
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Location/Qualifiers
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/gene="F9F8.1"
3070. .>5013)
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5589. .7932
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KSMPTEFADDSPYDLVSADGKQTVNSSEWTYFWEEQWD"
complement(5513...5597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="exon predicted by xgrail,
complement(2090. .2250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"exon predicted excellent_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1182 . .1357)
/note="exon predicted by
marginal_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon predicted by xgrail, 672. .752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        excellent_shadowexon"
355. .594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon predicted by xgrail,
complement(347. .408)
                                                                                                                                                 /note-"exon predicted by xgrail, quality excellent_shadowexon" join(5589. .5795,5897. .5929,6013. .6235,7467. .7932)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(3215. .3325,3565. .
4506. .4655,4800. .5013)
/gene="F9F8.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="exon predicted by xgrail, 2114. 2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="exon predicted by 1747. .1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="exon predicted by xgrail,
       /note="similar to nucleic acid binding protein Alfin-1 GB:AAA20093 [Medicago sativa]" join(5696. .5795,5897. .5929,6013. .6235,7264. .7387,
                                                                                                                                                                                                                                           complement (5527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F9F8.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3702"
/chromosome="III"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thaliana]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(13367. .13468)
/note="exon predicted by xgrail, quality marginal"
/note="exon predicted by xgrail, quality marginal"
/note="exon predicted by xgrail, quality marginal"
/note="exon predicted by xgrail, quality marginal"
complement()oin(13822. .14179,14261. .14398,14502. .14582,
14676. .14861,14941. .15033,15124. .15190,15272. .15361,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRTYEGYGSRIGVERGAILDWNDYYLHFLPLALKDENKWPSLYSNIREMNDEYGKEL
VKLGGRLWTILSSNIGLRAEQLQEAFGGEDVGACLTVNYPKCPQPELLIGLSPHSDP
GKMTILLPDDQVVGLQVRHGDTWITVNPLRHAFIVNIGDQIQILSNKKKKYDEHRYIV
NSEKERVSLAFFYNDKSDIPIQPMQQLVTSTMPPLYPPMTFDQYRLFIRTQGPRGKSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product "putative leucoanthocyanidin dioxygenase" 
/protein_id="AAF01507.1" 
/db_xref="G1:6016680" 
/tanslation="MUNLDEIKIESKTCLUDGEQEVKIDUMHMSDQDKNKIEIKNKSG 
LGEKWPEPIVRVQSLAESNLTSLPDRYIKPPSORPQTTIIDHQPEVADINIPIIDLDS 
LFSGNEDDKKRISEACREWGFFQVINHGVKPELMDAARETWKSFFNLPVEAKEVYSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note-"similar to leucoanthocyanidin dioxygenase GB:BAA20143 [Perilla frutescens]" complement(join(9426. .9674,10198. .10528,11098. .1491. ..1865))
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11491. .×11865))
/qene="r9p8.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="maaaavssnprtveeifkdysarraallraltkdvddfysqcdp
EKENICLYGHPNESWEVNLPAEEVPPELPEPALGINFARDGMQRKDWLSLVAVHSDCW
LLSVSFYFGARLNRNERKRLFSLINDLPTLFDVVTGRKAMKDNKPSSDSGSKSRNGTK
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/protein_id="AAF01506.1"
/db_xref="GI:6016679"
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/gene="F9F8.2"
                                                           /protein_id="aaf01508.1"
/bd_xref="G1:6016681"
/translation="manivisecgirplpriyTtprsnflsnnnkfrpslssssykts
/translation="manivisecgirplpriyTtprsnflsnnnkfrpslssssykts
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lghdcghgsfsndpklnsyvghllhssilvpyhgwrishrihqnhghvendeswhpm
                                                                                                                                                                                                                                                                                                         complement(join(13988. .14179,14261. .14398,14502. .14582, 14576. .14861,14941. .15033,15124. .15190,15272. .15361,
                                                                                                                                                                                                                                                                                                                                                                          /note=""identical to omega-3 fatty acid desaturase, chloroplast precursor GB:P46310 [Chloroplast Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                          complement(13822. .16380)
/gene="F9F8.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="exon predicted by xgrail,
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/codon_start=1
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                                        SEKTYNTLDKPTRFFRF¶LPLVMLAYPFYLWARSPGKKGSHYHPDSDLFLPKERKDVL
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12824. .12836
                                                                                                                                                                                                                       /product="omega-3 fatty acid desaturase, chloroplast
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Best Local Similarity 54.9%;
Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Hutzar, L., Rowley, D., Chen, S., Harman, P., Hicks, R., Huerta, M., Mason, S., Siepel, J., Zimmerman, M., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
Submitted (10-JUL-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC008017 116944 bp DNA PLN Arabidopsis thaliana chromosome I BAC F3N23 complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Chen, S., Harman, P., Hicks, R., Huerta, M., Mason, S., Siepel, J., Zimmerman, M., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskafa, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Tortumi, M., Yysotskafa, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and
Direct Submission
Submitted (15-JUL-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 943
                                                                                                                                        Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Chen, S., Harman, P., Hicks, R., Huerta, M., Mason, S., Siepel, J., Zimmerman, M., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 116944)
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JOURNAL
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Submitted (18-SEP-1999) DNA Sequencing and Technology Center, Submitted (18-SEP-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (bases 1 to 116944)
Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafl.H., Araujo, R., Huizar, L., Rowley, D., Brooks, S., Buehler, E., Chao, O., Dunn, P., Gonzalez, A., Khan, S., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriuni, M., Vyotskala, V., Yu, G., Ecker, J., Theologis, A. and Dayis, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jul 15, 1999 this sequence version replaced gi:5441915.
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HLIRETTAELPTYLANSLNSLRLEGQKTAAIEILQQFWQVPDWYVIVPGGNLGNIYAF
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/note="81% identical to threonine synthase [Arabidopsis thaliana] (gil4914408). Location of ests GBGF589 3' (gb|F15267) and GBGe175 (gb|226034)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(1333. .2271,2355. .2966))
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LVNASRCNYVNGFDAFFKIVRADGFKGLYRGFGISILTYAPSRAVWAASYSVAQRMVW
GGIGCYVCKKDEESGNNSTTMKPDSKTIMAVQGVSAAIAGSVSALITMPLDTIKTRLQ
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6030. .7079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKGFHMCKELGLVDRIPRLYCAQAANANPLYLHYKSGFKEDFNPLKANTIFASAIQIG
DPVSIDRAVYALKKSNGIVEEATEEELMDATALADSTGMFICPHTGVALTALMKLRKS
GVIGANDRTVVVSTAHGLKFTQSKIDYHSKNIKEMACRLANPPVKVKAKFGSVMDVLK
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complement(8272. .9661)
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/note="Unknown protein; Location of ests 205D12T7
(gb[H77203) and 205D12XP 3' (gb[AA605559)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYLKSNDK"
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/chromosome="I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLDGEDSSNNGKRGPSIGQTVRNLVREGGWTACYRGLGPRCASMSMSATTMITTYEFL
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LAKIDSWEGGSER I ITTENSELUSCEN WITEVECLIDENDALQVEKKLARGEPPS
DGFEROLF TRASRLAHGLISSALVARSHLSALVALDENBALQVEKKLARGEPPS
DGFEROLF TRASRLAHGLISSALVARSHLSALVALDENBYDELLIETEPRKWYGEILRA
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NLRELPELSTAVNLEELILESCTSLYQIPESINELYLKKLNSLWOGTKLENLINLNIEDIPE
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DVKIGSLAGIIGAGRYNLLDFCVEKCKSLGSLWGILSVEKSABGRNELLELSLENCKS
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KYLYAHGCESLEHVNFSSNHSFNHLDFSHCISLECTSDLVRDFMNEEYSQEAPFRLVC
ITKYSIASTNNMRTSWREDRIKLFKIKABRLVGFFYQIMVVCEKPFHLQFFAFSYN
WOCHGSRLYRINLRFNLYQSSEMMEDNNNRFYKWHHLVIVQIFTGIISAEIDEVQFES
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join(16543..16961,17058..17907)
/gene="F3N23.5"
/note="F3N23.5"
/note="Similar to N-terminal half of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYLPIFYGYKPSDYRYQEGSFATAFQSYDEADMIAEYVGGISSRLPRMKSTDLINLYG
MEAHMMKMTLLLNIGCEDEVHMIGIWGMGGIGKSTIAKCLYDRESRQFPAHCFLENVS
KGYDIKHLQKELLSHILYDEDVELWSMEAGSQEIKERLGHQKVEYVLDNYDKVEQLHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="massssssatrlrhydvflsfrgvdtrqtivshlyvalrnngvl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(12076. .12519,12613. .13851,13955. .14140, 14368. .15451,15672. .16057))
                                                                DDKKLELGDSISEEISRAIQNSTYALVILSENYASSWCLDELRMYMDLHLKNKIKVV PIFYCYDPSHYRHQTGSFTFDKYQDSKHUNKVTTWREALTQIASIAGKDFETCEDEAS MIEEIVKDISKKLLIMQPVDFSDIVGMNAHMERLSPLLSMDSENEVRMIGGIWGMGGIKTIAKCLFTDGSQGFPARCFLENVSKIYRKGGVSSLAEKFLSTTLGLSKKKMKGSGV KLGPQEIKARFGCRKVFVVLDNVDDMRQMHAFAQESSWEGPGSRIIITTRUKGLLNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPLTAKODGLVGMDRQMQTLYKLLDFKAAEEVRLIGIWGPGGIGKTTLARYAYEEISS
NEKVHYFVDKAEKICHQDRDLLKLLTEEGTTQGLDVGIDKIKSTFGHRKGLIVIDCVD
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LAEESKLAVVVVSESYPISVLCLNQLEKIVNSHSEGRLSILPIFYGVDPYNVRKQTGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistance protein (g1|2109275)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIQVPEPGDEIILCGVEHVGFVLK"
16543. .17907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Similar to disease resistance proteins"
/protein_id="AAD55631.1"
/db_xref="GI:5903073"
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(gi|3860165), RPP1-WsC (gi|3860167) and RPP1-WsA
(gi|3860163) [Arabidopsis thaliana]."
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GVRTVYEVKCMDNDAALQLFNQLAFKGALPPSELYEKLSIRASWLAQGLPVAIEAYGL
FFRRWTSLKEWDDALCRFIEAPDESVMEILKISYDGLEETDKNVFLHVACLFNGEPLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAD55632.1"
/db_xref="GI:5903074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"Similar to
                                                                                                                                                                                                                                                    /product-"Similar to downy mildew resistance protein RPP5"
/protein_id="AAD55633.1"
/db_xref="G1:5903075"
/translation-"MASSSSSPIWKYDVFLSFRGEDTRKNIVSHLHKQLYDKGVVTFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resistance protein
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RATTLLDDGVLQGCLGLKILAEKSLIEITASGYIKMHNLVDQTARAIVNQESMQRRHG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ipomoea nil receptor-like protein kinase (inrpkl) gene, complete
Bassett,C.L., Cohen,R.A., Nickerson,M.L. and Rajeevan,M.S. Direct Submission Submitted (12-NOV-1996) USDA, ARS, Appalachian Fruit Research
                                                                                                                                                            1 (bases 1 to 5033)
Bassett,C.L., Cohen,R.A., Nickerson,M.L. and Rajeevan,M.S.
Identification and Preliminary Characterization of an Unusual
Leucine-rich Repeat Receptor-like Protein Kinase from Morning
                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Convolvulaceae;
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ILAIFLFFEYEYAQGMPNLRKLDLSDSENLEQLDLSMAVNLEELTTQGCKRLKKIPES
ISYLTRLTTLVSYCEELASYITIRELMRSGRQIALFSGKEVETRSIAURSIGGNIH
IQMFWLDGNVDHLSFTTEQQGPDKLTKKEKQQAFGELTKREQQGEPKKTILCGFGSL
MRKGRKVKATSEFLDHEWMMQRDQLAFDNQQALEFSTERRACHOFLPEFHGQESVKA
QGKSQPTSKFHGFTSVDISRFYNSGSDGASFICCFSLSMFPCVKELILINLNIKVIFDDV
CGLKFLEKLDWSGNDFSTLPETMNGLPRLXYASFRNCCRLKALPALVQLTIKLSGCI
NLQSLLELSYAEQDCGRFQWLELWYDGCKSIRSILDQLRHFIKLSYLDLSSHEFEKLP
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HCFGLKRDEHLIAQFLNEGENEEESLGFAFFPGTEVPSYFDHIDKGKSLTIDLPQIWP
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511 taaagttgttgatgtctcaagcaatgatttgtgtgtggaacaatcccaacaaa
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                                                                        CTCAATTCCTTCCCAGCTAGGCAATTGCAGTCTTCTTGAACACATAGATCTGTCCTCCAA
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                                                                                                                              CAGCTTTACTGGTAATATCCCTGACACCCTTGGAGCTTTGCAGAATTTAAGGAACTTAAG
                                                                                                                                                      tgagcttgggaagcttgaacatttacagtatctagagctctacaaaaacaacatccaagg
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PPGIGNITSIREFGAFSCALSGFIPSCFGQLTKLDTLYLAGHIFSGRIPPEIGKCKSM
IDLQIAQNOLEGEIPGELGMLSQLQYLHLYTINNLSGFPVLSIWKIQSLQSLQLYQNIL
SGELPVDMTELKQLVSLALYENHETGVIPQDLGANSSLEVLDJTRNMFTGHIPPILCS
QKKLKRLLLGYNYLEGSVPSDLGGCSTLERLILEENNLRGGLPDFVBKQNLLFFDLSG
NNFTGPIPPSLGNLKNVTAITYLSSORSTIPPELGSLVKLEHLNJSHNILKGILPSE
LSNCHKLSEIDASHNLLMGSIPSTLGSSLTELTKLSLGENSFSGGIPTSLFQSNKLLML
QLGGNLLAGDIPPVGALQALRSINLSSNKLNGQLPIDLGKLKMLEELDVSHNNLSGTL
RYLSTIQSLTFINISHNLFSGPVPPSLTKFLNSSTSFSGNSDCLTNCPADGLACPES
SILRPCNMOSNTGAGGLSTLGTAMIVLGALFITLFSAFLFLHKKLVFTGIKNGSV
SMUREIETIGKVFHRNLLKLEEFWLREXGLHFITLYTYMENGSLBDILGTAVITORS
SMUREIETIGKVFHRNLLKLEEFWLREXGLHTYTYMENGSLBDILGETNYTKELDS
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SIPSNTVQGTIGYMAPENAFTTVKSRESDVYSYGVVLLELITRKKALDPSFNGETDIV
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TIQSWIASDSTPCSWLGYBCDBRQFVDTLNLSSYGISGEFGPEISHLKHLKKVVLSGN
GFFGSIBSQLGNCSLLEHEIDLSSNSTFGLIPSDGFGFEISHLKHLKKVVLSGN
LSIPHLETVYFTGNGLNGSIPSNIGNKSELTTLWLDNQFSGPVPSSLGNITTLQELY
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/gene="inrpk1"
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/protein_id="AAB36558.1"
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/cultivar="Violet"
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Best Local Similarity
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2586 CTATTCTTTATCTTTACGAGAACTATTTAACTGGTGTCATTCCCCCGGAACTAGGCAACA 2645
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                                                                                                          | totacaaaacaacatccaaggaactataccttccgaacttggaaatctgaagaatctca 368
                                      tcagcttggatctgtacaacaacaatcttacagggatagttcccacttctttgggaaaat 428
                                                                                     TGAGTAACAAACTTACCGGTTCAATTCCTTCCTTAGGAAATCTCAAGAATTTGA
                                                                                                                                                                       ATCTAACTGGTGGCATTCCCCCGAAACTAGGCAACATAGAATCCATGATCGATTTAGAGT
                                                                                                                                                                                                                                                             165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Street, Albany, CA 94710, USA
On Feb 11, 2000 this sequence version replaced g1:6693723.
The sequence is of BAC F14D7 from Arabidopsis thaliana chromosome
1. The sequence does not represent the sequence of the entire
insert of this clone. It is shorter by 6954 bp because we submit
only the unique sequence of the clone. However, in order to
facilitate the joining of overlapping clones in the future for
creation of larger contigs, we provide small overlaps (200 bp)
between overlapping sumbitted clones. The 5' end of this sequence
overlaps by 200 bp to the 3' end of the sequence of the clone
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Liu,S.X., Sakano,H., Yu,G., Lee,J.M., Lenz,C., Pham,P., Toriumi,M., Chin,C., Chiou,J., Choi,E., Chung,M., Gonzalez,A., Howng,B., Liu,A., Vaysberg,M., Altafi,H., Brooks,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N.F., Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R., Federspiel,N.A. and
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Theologie *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Submitted (09-FEB-2000) Plant Gene Expression Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana chromosome 1 BAC F14D7 sequence unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
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Pred. No. 4.1e-12;
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              prediction programs including GRAII (available by annotation), Genes including GRAII (available by annonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database nhtml), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html).

Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, to other proteins are named as funknown, proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are predicted by tRNAscan-SE (Sean Eddy, http://genome.wusti.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://genome.wusti.edu/eddy/tRNAscan-SE/).
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Arabidopsis thaliana chromosome I
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The Institute for Genomic Research
9712 Medical Center Dr.
Rockville, MD 20850, USA
e-mail: xiln@ttgr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (08-DEC-1999) The Institute for Genomic Research,
Submitted (08-DEC-1999) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
On Dec 8, 1999 this sequence version replaced g1:6102640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin, X. and Kaul, S.
Direct Submission
Submitted (14-OCT-1999)
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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The orientation of the sequence is from SP6 to T7 end of the BAC
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ittp://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions
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), USA, xlin@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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exons by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence that are not annotated as genes but have predicted GRAIL are annotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1378. .1581

/note="exon predicted by xgrail, quality good_shadowexon" complement(1509. .150)

/note="exon predicted by xgrail, quality marginal" complement(10in(c1655. .1777,1908. .2135,2258. .2581, 2679. .2963,3052. .>3429))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1271. .1354
/note="exon predicted by xgrail,
complement(1356. .1475)
/note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon predicted by xgrail,
complement(393. .453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVKFMAREILILRRLNHPNIIKLEGLITSKLSCNIQLVFEYMEHDLTGLLSSPDIKFT TPQIKCYMKQLLSGLDHCHSRCVMHRDIKGSNLLLSNEGILKVDEGLANESNSSGHK KKPLISRVVTLMYRPPELLLGAFDLSGSVDLMSVGCVFAELLLGKPILRGRTEVEQLH KIFKLCGSPPEDYMKKSKLPHAMLFROQUTVDSCLRETLKDLSETEINLIETLLSIDP HKRGTASSALVSQYFTTKPFACDPSSLPIYPPSKEIDTKHRDEAARSVISFIT" complement (4069...4131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MGCVSSKQTVSVTPAIDHSGVFKDNENECSGSGRIVVEDPPRPT
LKKLVSWRSRSGKRRSQKSGSELGSESGRASDSLSFRLGNVSRYLEAEQVAAGWPAWL
SNVAGEAIHGWVPLRSDAFEKLEKIGQGTYSNVFRAVETETGRIVALKKVRFDNFEPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to p58 protein kinase GB:AAB59449 [Homo saplens]; contains Pfam profile: PF00069 Eukaryotic protein kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(<1655. .>3429)
/gene="F1M20.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         marginal_shadowexon'complement(229. .281
                                                                                                                                                                                                                                                                                                                                                                       /note="similar to dolichyl-phosphate mannosyltransferase polypeptide 2 GB:4503365 [Homo sapiens] (regulator of dolichol phosphate-mannose synthesis: EMBO J 1998 Sep 1;17(17):4920-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="exon predicted by xgrail, quality excellent" complement()oin(<4608. .4760,4885. .>4974))
/qene="fix20.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative protein kinase"
/protein_id="AAF15905.1"
/db_xref="GI:6539235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="exon predicted by xgrail, 1271. .1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="exon predicted by xgrail,
complement(744. .1286)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="F1M20"
138. .269
                              /note="exon predicted by xgrail, quality excellent"
complement(<5342. .>7603)
                                                                                     /translation~"MELADRAVGLLLSSISLSIFTYYTFWVIILPFVDSDHFIHKYFL
PQDYAILVPVFAGIALLSLISVFIGMVWLKSKKKKA"
complement(5111 .5190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(<4608. .>4974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F1M20.
/codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(1655..1777,1908..2135,2258..2581,
2679..2963,3052..3429))
/qene="$1M20.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="I"
/map="mi425"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                      /product="putative dolichyl-phosphate mannosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"F1M20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar≖"Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Arabidopsis thaliana"
                                                                                                                                                                       /protein_id="AAF15906.1"
/db_xref="GI:6539236"
                                                                                                                                                                                                                                                                                                                   /gene="F1M20
                                                                                                                                                                                                                                                                                                                         (join(4608. .4760,4885. .4974))
20.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality excellent"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality excellent"
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Query Match
Best Local Sim
Matches 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                              Similarity
   Conservative
                                                                                                                            /translation="Mariavagdsldsdrevilslksylesrnpqnrglytewkmenq
DVVCQwpgiictporsynginltdstisgeleknetaelityldlsrntiegeled
DLSRchikkhluselslegishtevldsikhitietslydeskiplityldlyrn
DLSRchikkhluselslegishtevldsikhitietslydestyld
DLSRchikkhluselslegishtevldsikhitietslydbisknitetslyd
NLSTINNETGRIDDIFNGCRILKYVDESSNRESGEVETGRETUNESGLISAISA
SMFRGNCTLOMLDLSGNAFGGEPFGQVSNCQHLAVLJHIMGKRETGRITAEIGSISSLK
GLIGANUFTSRDIEDETLAHLTHLJYFLDLSRNKFGGDIDEIFGRETOKYLTULHAVSVY
GGINSSNILKLENLSRLDLGYNNESGQLPTEISQIQSLKFLILAYNNESGDIPQEYGN
MGGLOALDLSFNKLTGSIPASFGKLTSLLWLMLANNSLSGEIFREIGNCTSLLWENNA
NNOLSGREHPELTRMGSNESFFFEVNROMDKRIAGSGECLAMKRWITHAEFPPFNYY
AILTKKSCRSLMGHYLKGYGLFPVCSAGSTVRTLKISAYLQLSGNKFSGEIFASISQN
DRLSTLHLGFNEFEKLPEIGQLPLAFINLTRNESGSIPAGIGLMKCLQNLDLSFN
NTSGNETSLNDLNELSKNISTWFFISGSIFTGNOTAATEJNGSFLGNFLKEPSEFN
QSGNNTRKISNGVLGNERFTLLLIWISLALALAFIACLVYGGIVLAWVKASREAEIDL
LDGSKKILVHEYMKLQREGTEAKEFFRAEMEYLSANAFGDWAHFNLVPLLYGWCL
DGSKKILVHEYMKLQREGTEAKEFFRAEMEYLSANAFGDWAHFNLVPLLYGWCL
DGSKKILVHEYMKLQREGTEAKEFFRAEMEYLSANAFGDWAHFNLVPLLYGWCL
DGSKKILVHEYMGGGSLEELITDKTKLQWKKRIDIATDVARGCUFFGHHECYPSIVHBD
DGSKRETLYHEYMBGGGSLEELITDKTKLQWKKRIDIATDVARGCUFFGHHECYPSIVHBD
DGSKRILVHEYMBGGGSLEELITDKTKLQWKKRIDIATDVARGCUFFGHHECYPSIVHBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /TIADS LATION MASKETGMF SLAGELASLIVEESSSHYDDDSKPRSMELKRSLEL
RLKKRVKEDCINGKFSDLLKKVIARPETILDAXIDCIRLNSWYKSITERNGSVAPDSIAE
ELSGSVEDVASWTFS IVARDKTKEVLVLPSVALKVVQEAIR IVLEVVESPHFSKISHS
ELSGSVEDVASWTFS IVARDKTKEVLVLPSVALKVVQEAIR IVLEVVESPHFSKISHS
CRSGRGRASALKYINNISRSDMCFTLSLNKKLDVSVEENLLSVMEEKVEDSSLSILL
RSMFEARVLNLERGGFFKCHGLPQEGVLSRVLANIYLDRFDHEFYRISMRHBALGLDS
KTDEDSPGSKLRSWFRQAGEQGLKSTTEQDVALKVYCCFPWDEIYFSVGAWRKKEX
KTDEDSPGSKLRSWFRQAGEQGLKSTTEQGLVALKVYRESPFYKAVHKLKEX
VRLFALQKEEAWTLGTVRIGKKWLGHGLKKVKESEIKGLADSNSTLSQISCHRKAGME
TDHWYKILLRIWMEDVLRTSADRSEEFYLSKHVVEFYVPQELEADAFYKFQNAAAAVVS
SETANLEALLPCYGSHDREVFFGDVVAFNATAIGRKLKFKYGLITAAKKRIHEMEIEKR
TGAGILDWYSGLVRRWVIWYEGCSWFDEIKALINQIRWSCIRTLAAKKRIHEMEIEKR
LDLELSTIPSAEDIEQEIQHEKLDSPAFDRDEHLTYGLSWSCLCLLSLARIVSESRPC
LDLELSTIPSAEDIEQEIQHEKLDSPAFDRDEHLTYGLSWSCLCLLSLARIVSESRPC
LDLELSTIPSAEDIEQEIQHEKLDSPAFDRDEHLTYGLSWSCLCLLSLARIVSESRPC
LDLELSTIPSAEDIEQEIQHEKLDSPAFDRDEHLTYGLSWSCLCLLSLARIVSESRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="exon predicted by 8771. .8821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"similar to brassinosteroid insensitive 1 GB:AAC49810 (putative receptor protein kinase); contains Pfam profiles: pF00560 Leucine Rich Repeat (17 repeats), pF00069 Eukaryotic protein kinase domain" 10992. .14231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marginal_shadowexon"
9421. .9528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               marginal_shadowexon"
8935. .9008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCFVIGCSMAAPAVYTLHAMERQKFPGWKTGFSVCIPSSLNGRRIGLCKQHLKDLYIG
QISLQAVDFGAWR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="contains Pfam profile: PF01348 Type II intron maturase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(<5342. .>7603)
/gene="F1M20.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(5342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative rec
/protein_id="AAF15908.
/db_xref="GI:6539238"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="exon predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative type
/protein_id="AAF15907.1"
/db_xref="GI:6539237"
                                                                                                             VKASNVLLDKHGNARVTDFGLARLLNVGDSHVSTVIAGTIGYVAPEYGQTWQATTRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F1M20.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="F1M20.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <10992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F1M20.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family-"POLY_A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'codon_start=1
                           10.0%;
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0;
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                           Score 79.2;
Pred. No. 6
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .7603)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by xgrail,
                           6.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          II intron maturase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xgrail,
                                                      DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality good"
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                                                   Length 134402;
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pathogen re Cf-9 cDNA. pathogen re Cf-9 gene.

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                                   O. longistaminta x
Maize Ka21 gene DT
Tomato polygalactu
Maize Ka21 gene DT
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Arabidopsis steroi
Pear polygalacturo
Rice Xa21 disease
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Tomato pathogen re
Arabidopsis thalia
Daucus carota SERK
CF-5 pathogen resi
CF-5 pathogen resi
O. sativa Xa21 gen
CF-5 pathogen resi
O. longistaminata
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O. longistaminata
Tomato Xa21 clone
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20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S.
WPI: 98-086529/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V06588 standard; cDNA to mRNA; 788 BP.
V06588;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clone.
receptor kinase; apomixis; apomictic; seeds; production; plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Arabidopsis Luccation/Qualifiers
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P-PSDB; W47020.

Production of apomictic seeds - useful in plant breeding Claim 28; Pages 79-80; 123pp; English.

The sequence is that of an EST clone showing high homology SERK LRR (leucine-rich repeat) sequences.

Sequence 788 BP; 234 A; 191 C; 156 G; 207 T;
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SUMMARIES

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(NOVS) NOVARTIS AG.
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WPI; 98-08559/08.
P-PSDB; W47022.
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The sequence is that of an EST clone showing high SERK LRR (leucine-rich repeat) sequences.
Sequence 1063 BP; 313 A; 242 C; 206 G;
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(NOVS) NOVARTIS AG.

De Vries SC, Hecht VFG, Schmidt EDL, Van
WPI: 98-086529/08.

P-PSDB; W47019.

Production of apomictic seeds - useful in
Claim 28; Pages 75-77; 123pp; English.
The sequence is that of an EST clone show
SERK LRR (leucine-rich repeat) sequences
                                                                                                                   v-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST receptor kinase; apomixis; apomictic; seeds; plant breeding; leucine-rich repeat; ss. Arabidopsis thaliana.
                                                            20-NOV-1997.
13-MAY-1997;
14-MAY-1996;
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V06588;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clone.
receptor kinase; apomixis; apomictic; seeds; produc
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
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20-WOV-1997.

20-WOV-1997.

R 14-MAY-1996; GB-010044.

R (NOVS) NOVARTIS AG.

I De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

R WPI; 98-086529/08.

R P-PSDB; W47018.

T Production of apomictic seeds - useful in plant breed Claim 28; Pages 71-73; 123pp; English.

C SERK LIRK (leucine-rich repeat) sequences.

Sequence 1106 BP; 331 A; 258 C; 206 G;
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13-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-08529/08.
P-PSDB; W47021.
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Arabidopsis thaliana SERK LRR homologous EST receptor kinase; apomixis; apomictic; seeds; plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Production of apomictic seeds - useful in plant br Claim 28; Pages 83-84; 123pp; English.
The sequence is that of an EST clone showing high SERK LRR (leucine-rich repeat) sequences.
Sequence 894 BP; 270 A; 163 C; 176 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V06589 standard;
V06589;
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ccctagagcactcactgcaatccccaagccttaaagttgttgatgtctcaagcaatgattt
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/note= "shows high homology to
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Pred. No. 1.8e-99;
0; Mismatches 110
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                                                                                                                 Production of apomictic seeds - useful in plant breeding Claim 27; Pages 91-95; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing that the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity plant proyeny. This is useful in plant can be developed into plant proyeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding programs allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
                                                   Matches
                                                                 Query Match
Best Local :
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(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG,
WPI; 98-086529/08.
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                                                                   Similarity
                                                    Conservative
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; apomixis;
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195. .2072
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                                                   Score 211.8;
Pred. No. 2.8e
0; Mismatches
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Production of apomictic seeds - useful in plant breeding
Production of apomictic seeds - useful in plant breeding
Production of apomictic seeds

CC In may be used as part of a method of producing apomictic seeds

CC comprising: (a) transforming plant material with a nucleotide

CC sequence encoding a protein which in active form in a cell or

CC ell membrane renders the cell embryogenic; (b) regenerating

CC the transformed material into plants or carpel-containing

CC plant parts; and (c) expressing the sequence in the vicinity

CC of the embryo sac. The apomictic seeds and embryos thus produced

CC can be developed into plant progeny. This is useful in plant

CC can be developed into plant progeny. This is useful in plant

CC can be developed into plant progeny. This is useful in plant

CC can be developed into plant progeny. This is useful in plant

CC can be developed into plant progeny. This is useful in plant

CC can be developed into plant provement and cultivar development in

CC capomictic plant. Apomixis provides for true-breeding, seed

CC apomictic plant. Apomixis provides for true-breeding, seed

CC propagated hybrids and could shorten and simplify the breeding

CC process so that selfing and progeny testing to produce and/or

CC stabilise a desirable gene combination could be eliminated.

CC apomixis allows plant breeders to develop cultivars with

CC specific stable traits for such characteristics as height,
                                                                                                                                                                                                                                                                                                                                                                14-MAY-1996; GB-010044.
(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG,
WPI; 98-086529/08.
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V06571;
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Sequence
DNA encoding plant morphogenesis regulatory protein - useful to yield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 17pp; Japanese.

The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to yield a plant with, e.g. short stems or altered inflorescence. The MRP acts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant.

Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;
                                                                                                                                                                           24-AUG-1995; 216187.
24-AUG-1995; JF-216187.
24-AUG-1995; JF-216187.
(MITS-) MITSUI GYOSAI SHOKUBUTSU (CHIK-) ZH CHIKYU KANKYO SANGYO G WPI: 97-206629/19.
                                                                                                                                                                                                                                                                                                                                                        10-JUN-1997 (first entry)
Arabidopsis thaliana plant morphogenesis regulatory protein (
Plant; morphogenesis; regulation; short; stem; alteration;
Plant; morphogenesis; regulation; expression; transformation;
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increase; control; form; l
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17-JUL-1998; U14841.
13-AUG-1997; US-910386.
(REGC) UNIV CALIFORNIA.
Hulbert SH, Richter T, Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant
Oryza
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                                                                                                                                                                                                                                  New RRK polynucleotides and nucleic acid constructs - used for generating transgenic plants resistant to Xanthomonas Claim 1; Page 52-53; 67pp; English.

This invention describes a method for conferring disease resistance in plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor kinase-like protein (RRK) Xa21 multigene family. Such genes from cassava, maize and tomato are also described. The genes and proteins cabe used for enhancing resistance to Xanthomonas in a plant, preferably
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23-NOV-1995.
11-MAY-1995; G01075.
11-MAY-1994; GB-009394.
23-DEC-1994; W0-G02812.
31-MAR-1995; GB-006658.
07-APR-1995; GB-007232.
                                                                                                                                                                                                                                                                                                                                                                                     Increasing plant pathogen resistance by induction of varisgation—may lead to acquired resistance to a broad range of pathogens.

Claim 9; Page 85-87; 131py; Engilish.

T06307 is a tomato pathogen resistance gene Cf-2.2 partial cDNA clone. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.2 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosportum fulvum.

C.fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 3573 BP; 1032 A; 654 C; 664 G; 1223 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Partial tomato pathogen resistance gene Cf-2.2 cDNA Pathogen resisitant; Cf-2.2; tomato; C.fulvum; Avr 4
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                                                                                                                                                                                                                                                AACAACTTGTCTATGTTGTATCTTTACAATAATCAGCTTTCTGGCTCTATTCCTGAAGAA 1846
                                                                                                                                                                                                                                                                       aaccgcgtcactcgtgtggatttgggggaattcaaacctctctggacatctttgcgcctgag
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CCGAGAAACAATTTGAAGGGAAAAGTTCCGCAATGTTTGGGTAATATCAGTAACCTTCAG
                      ATTCCTGCTTCATTTGGCAATATGAGAAATCTGCAAGCTCTGATTCTCAATGATAACAAT
                                                                                                                                           CTCATTGGGGAAATTCCTTCATCTGTGTGCAATTTGACATCACTGGAAGTGTTGTATATG
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Pred. No. 8.5e-12;
0; Mismatches 171
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Best Local Similarity 50.4
Matches 174; Conservative
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11-MAY-1994; GB-009394.

23-DEC-1994; WO-G02812.

31-MAR-1995; GB-006658.

07-APR-1995; GB-007232.

(GATS-) GATSEY CHARITABLE F.

Hammond-Kosack KE, Jones D

WPI; 96-010999/01.
                                                                                                                                                                                                                                                                              Increasing plant pathogen resistance by induction of variegation - may lead to acquired resistance to a broad range of pathogens. Claim 9; Page 80-83; 131pp; English.

706306 is the tomato pathogen resistance gene Cf-2.1. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.1 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulvum. C.fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 6471 BP; 2073 A; 1106 C; 1122 G; 2170 T;
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P-PSDB;
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23-NOV-1995.
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Pathogen resisitant; Cf-2.1; tomato; C.fulvum; Avrleaf mould; variegation; ds.
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CTCATTGGGGAAATTCCTTCATCTGTGTGCAATTTGACATCACTGGAAGTGTTGTATATG 3710
               ataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtacaacaacaat
                                                                                                                                                            AACAACTTGTCTATGTTGTATCTTTACAATAATCAGCTTTCTGGCTCTATTCCTGAAGAA
                                                                                                                                                                                       aaccgcgtcactcgtgtggatttggggaattcaaacctctctggacatcttgcgcctgag
                                                     ATTCCTGCTTCATTTGGCAATATGAGAAATCTGCAAGCTCTGATTCTCAATGATAACAAT
                                                                                                          ATAGGTTACTTGAGTTCTCTTACTTATCTATCTTTGGGTAATAACTCTCTTAATGGACTT
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5015. .647
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1677. .
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1. .1676
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Pred. No. 1.1e-11;
0; Mismatches 171;
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Production of apomictic seeds - useful in plant breeding Claim 26; Pages 64-67; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel containing plant material and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomixic provides and could shorten and simplify the breeding programation or containing the provides of the case that sexual plants are available as crosses with the case that sexual plants are available.
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20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-0100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor kinase; apor
plant breeding; ds.
Arabidopsis thaliana
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(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG,
WPI; 98-086529/08.
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5295. .5803
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3851. .39
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apomixis; apomictic;
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                  20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-086529/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 4081 Bp; 1120 A; 770 C; 785 G; 1406 T;
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98-086529/08.
)B; W47013.
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3851. .3979
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Pred. No. 1
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.4e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Production of apomictic seeds - useful in plant breeding Claim 21; pages 40-46; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant to breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed in the could stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
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Best Local Similarity
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20-MAY-1998
CF-5 pathoge
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20-NOV-1997.
08-MAY-1997; G
24-SEP-1996; G
09-MAY-1996; G
Tomato gene Cf-5, confers resistance to Cladosporium fulvum - useful for production of transgenic plants resistant to pathogens e.g. tomato leaf mould C. fulvum in tomatoes Claim 3; Fig 1a; 75pp; English.

This sequence is an example of the polynucleotide of the invention, a sequence is an example of the polynucleotide of the pathogen resistance on a plant. It is one of two two confer pathogen resistance against the pathogen cladosporium fulvum-5. Transgenic plants can be produced by incorporate the gene into plant cells; and regenerating plants from the cells; assexually or sexually produced offspring can also be subsequently
                                                                                                                                                                                                 24-SEP-1996; GB-019924.
09-MAY-1996; GB-0096B1.
(INNE-) INNES CENT INNOVATIONS LTD JOHN.
DIXON MS, Hatzixanthis K, Jones DA, Jone
MPI; 98-008895/01.
                                                                                                                                                                                    P-PSDB; W41309
                                                                                                                                                                                                                                                                                                                                                                                                                                          CF-5 pathogen resistance gene variant #1
Tomato; CF-5 pathogen resistance gene; C
tomato leaf mould; Phytophthora resistan
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                       resistance
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.7e-11;
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                                      incorporating
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Best Local S
Matches 172
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20-ROV-1997; G01249.
08-MAY-1997; G01249.
24-SEP-1996; GB-019924.
09-MAY-1996; GB-009681.
(INNE-) INNES CENT INNOVATIONS LTD JOB DIXON MS, HALZIXANTHIS K, JONES DA, JC WPI; 98-008895/01.
P-PSDB; W41310.
Tomato gene Cf-5, confers resistance to Cladosporium fulvum - usef for production of transgenic plants resistant to pathogens e.g. tomato leaf mould C. fulvum in tomatoes

Claim 6; Fig 1b; 75pp; English.

This sequence is an example of the polynucleotide of the invention is able to confer pathogen resistance on a plant. It is one of two CF-5 gene variants, which offer resistance against the pathogen Cladosporium fulvum-5. Transgenic plants can be produced by incorp the gene into plant cells and regenerating plants from the cells; assaually or sexually produced of the gene in plant cells can confer pathoge
                                                                                                                                                                                                                                                                                                                                                                                                  CF-5 pathogen resistance gene variant #2.
Tomato, CF-5 pathogen resistance gene, Clad
tomato leaf mould; Phytophthora resistance;
Lycopersicon pimpinellifolium.
Lycopersicon pimpinellifolium.
Lycopersicon pimpinellifolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          produced. Expression of the gene in plant cells can confer pathogen resistance on a plant e.g. to tomato leaf mould (C. fulvum) in tomatoes. Oligonucleotides with sequences complementary to the gene or fragments of it, are useful in anti-sense techniques to reduce gene expression. The nucleic acids/polynucleotides are useful as hybridisation probes to identify other genes/fragments conferring pathogen resistance on plants e.g. Phytophthora resistance in potatoes. Homologies between Cf-5 and Cf-9 may be used to identify further resistance genes of this class. Sequence 3979 BP; 1217 A; 717 C; 698 G; 1347 T;
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V14519;
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pathogen resistance gene; Cladosporium
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 653. .3560
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/product= CF-5
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Pred. No. 1.6e-11;
0; Mismatches 169
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                                                                                       invention,
one of two
         pathogen
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Search completed: June 23, 2000, 22:53:17 Job time: 40593 sec

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US-08-587-680A-1
US-08-587-680A-1
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Sequence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	•	Sequence 16, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 22, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Patent No. 5340934

ALIGNMENTS

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Sequence 3, Application US/08567375
Patent No. 5952485
Patent No. 5952485

GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANTON: Disease Resistance in Plants
CORRESSEE: Townsend and Townsend and Crew Lip
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: Galifornia
COUNTRY: San Francisco
STATE: Galifornia
COUNTRY: USA
ZIP: 9411-3834
COMPUTER: EDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CIASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/475,891
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APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
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; LOCATION: Join(1...2676, 3520...3918)
; OTHER IMFORMATION: /product= "xa-21"
US-08-567-375-3
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GENERAL INFORMATION:
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Best Local Similarity 50.3%;
Matches 156; Conservative
            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTACTGAACTTAATATCTTACTGCTCGGCACCAACAATTCAGTGGTTGGATACCATAC 1398
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                                                                                                                                                                                                                                                                                                                                                                                                  94111-3834
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US 60/004,645
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Pred. No. 7.1e-11;
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                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-475-891A-3
                                                                                                                                                                                                                                                                               Sequence 3, Application US/08475891A Patent No. 5859339
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Best Local Similarity
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TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                              APPLICANT: Ronald, Functions
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
TITLE OF SECUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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PRIOR APPLICATION DATA:
APPLICATION UNDER: US 0
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM
                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
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                    COUNTRY:
ZIP: 941
                                                    STREET: Two Embarcac
CITY: San Francisco
STATE: California
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                    94111-3834
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                                      USA
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Pred. No. 7
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SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:

Release #1.0, Version

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0

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REFERENCE/DOCKET NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0237(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5992 base pairs
TYPE: nucleic acid
STRANDEDNESS: -1--
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                                                                     Sequence 3, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
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FILING DATE: 06-7UN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-7AN-1995
ATTORNEY/AGENT INFORMATION:
 APPLICANT:
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                                   APPLICANT:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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156;
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TOPOLOGY: linear
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Similarity 50.3%;
56; Conservative
POWELL, Ann
STOTZ, Henrik
                                 BENNETT, Alan
LABAVITCH, John M.
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RMATION: /product= "RRK-B"
RWATION: /note= "Ra21 Xanthomonas spp. disease
RWATION: resistance gene RRK-B from rice (Oryza
RWATION: sativa)"
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Pred. No. 9.1e-11;
0; Mismatches 154;
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US-08-238-163-3
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian. Ferial
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Best Local Similarity 50.5%;
Matches 196; Conservative
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
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LENGTH: 2075 base pairs
TYPE: nucleic acid
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REGISTRATION NUMBER: 34,774
REFERENCE_DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    171 ttgttaatccttgtacctggttccatgtcacctgtaaccaagacaaccgcgtcactcgtg
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932 ATCGTAACAAACTCACCGGAACAATACC
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ZIP: 94105-1493
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STATE: California
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                                                                                                                                                                                                                             ttggaaatctgaagaatctcatcagcttggatctgtacaacaacaatcttacagggatag
                                                                                                                                                                                                                                                                         ATCTCGAAACATTGGAATTTCATCATGTTACTAATCTCACCGGAACAATTCCACCTGCAA 751
                                                                                               tgacggggccaatccctagagcactcactgcaatcccaagccttaaagttgttgatgtct 527
                                                                                                                                                                                                       TTGCGAAGCTCACAAATCTCAAAATGTTAAGGCTCAGCTTCACTAACCTTACAGGTCCGA 811
                                                                                                                                                                                                                                                                                                                                             TCACCGTCTTCCAAGCCAATATCTCCGGCCAAATTCCGGCAGCCGTCGGAGACCTTCCAT 691
                             caagcaatgatttgtgtggaacaatccc
                                                                TTACCGGAACAATCCCTTCTTCCCTCTCAGCTTCCGAATTTGCTAGCGATGTACTTAG
                                                                                                                                    E: Townsend and Townsend Khourie and Crew Steuart Street Tower, One Market Plaza
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421..1401
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Pred. No. 3.3e-09;
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959
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US-08-587-680A-24

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Best Local Similarity 45...
144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
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APPLICANT: Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: sinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE, TOUBER: 023070-058940US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/373,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITPLE OF INVENTION: Proceduted ....
TITLE OF INVENTION: Disease Resistance
TITLE OF CONTENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                     310
                                                                                                                                                                                           250 cctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagtatctagagct 309
430 gaagtctctggtctttttacggcttaatgacaaccgattgacggggccaatccctagagc 489
                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                           cagcttggatctgtacaacaacatcttacagggatagttcccacttctttgggaaaatt 429
                                                                                                                              ctacaaaaacaacatccaaggaactataccttccgaacttggaaatctgaagaatctcat 369
                                                                                                   AACTGGAAATGGTTTCTCAGGTGATATCCCCTTCTGATATTGGCAGACTAAAGAGCATCTT 137
                                                                                                                                                                    CTTGTCTGGTGCACTTCCTAGTGCTATTGGAAACTATTCAGGGCTGAAGAATCTTGTGTT 77
                                   AAAGCTGGACCTGAGTAGAAACAACTTCTCTGGCACAATCCCTCCTCAGATTGGTAACTG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24,
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                                                                                                                                                                                                                                                                                                                                     cDNA (partial)
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Pred. No. 1.5e-08;
                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                    Length 1554;
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US-08-238-163-1
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; OTHER INFORMATION: /standard_name= "Pear PGIP cDNA" US-08-238-163-1
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                                                                                                                                                                                       Query Match 7.0%;
Best Local Similarity 51.4%;
                                                                                                                                                                         Matches 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rele-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 03-MAY-199
CLASSIFICATION: 800
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Bastlan, Kevin L.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PLANT INHIBITORS OF TITLE OF INVENTION: POLYGALACTURONASES A
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                                      402
                                                                                                                         241 gaattcaaacctctctggacatcttgcgcctgagcttgggaagcttgaacatttacagta 300
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                                                                     301
361 gaatctcatcagcttggatctgtacaacaacaatcttacagggatagttcccacttcttt 420
                                                                                                     342 GCAACCCAATCTCACTGGCCCAATCCAACCCGCCATTGCCAAGCTCAAAGGACTCAAGTC 401
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1058 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                               NAME/KEY:
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                                                          totagagototacaaaaacaacatocaaggaactatacottccgaacttggaaatctgga 360
                                      TCTCAGGCTCAGCTGGACCAACCTCTCAGGCTCTGTCCCTGACTTCCTCAGCCAACTCAA
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STOTZ, Henrik
                                                                                                                                                                          Conservative
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Tower, One Market Plaza
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                                                                                                                                                                                         Score 55.4;
Pred. No. 1
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                                                                                                                                                                          Mismatches
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RESULT 7
US-08-475-891A-1
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FILING DATE: 06-JUN-1995
CLASSIETCATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BASTIAN, Kevin L.
REGISTRATION NUMBER: 02370-05891
FELEPHONE: (415) 576-0200
FELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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                                                                                      Matches 165;
                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ronald, Pameta (APPLICANT: Wang, Guo-Liang APPLICANT: Song, Wen-Yuang
      2735
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 ccctagagc 489
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                          231 tggatttggggaattcaaacctctctggacatcttgcgcctgagcttgggaagcttgaac 290
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                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: join(1648...4383, 5178...5513)
OTHER INFORMATION: /product= "RRK-F"
OTHER INFORMATION: /note= "xa21 Xanthomonas spp. disease
OTHER INFORMATION: resistance gene RRK-F from rice (Oryza
OTHER INFORMATION: sativa)"
                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
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STATE: California
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TGGACTTGGGAGAAAATAACCTGGGGGGAGTTCTTCCTAATTCGTTTTCCAATCTTTCCA 2794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                      Similarity
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                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                      7.0%;
                                                                               Score 55.4; DB 3;
Pred. No. 4.5e-08;
0; Mismatches 161;
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                                                                                                                       Length 6256;
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                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
APPLICATION NUMBER: US 08/373,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend
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                                                                                                                                                       REGISTRATION NUMBER: 34,774
REFERENCE/COCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                     FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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    MOLECULE TYPE:
                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/O FILING DATE: 04-DEC-1995
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                       TOPOLOGY: 11
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                                                    i: 6256 base pairs nucleic acid
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Song, Wen-Yuang
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                         Linea
                                                                                                                                                                                                                                                                        UMBER: US 08/373,375
17-JAN-1995
DNA (genomic)
                                       single
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RESULT 9
US-08-587-680A-1
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Best Local Sin
Matches 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UNBER: U$5/08/587,680A FILING DATE: 17-JAN-1996 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NOBER: U$ 08/373,375 FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTED 27

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

ADDRESSEE: Townsend Townsend and Crew LLP

ADDRESSEE: Townsend Townsend and Crew LLP
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NAME/KEY:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
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                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                STATE: California
                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
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RMATION: /product= "RRK-F"
RMATION: /note= "Xa21 Xanthomonas spp. d:
RMATION: resistance gene RRK-F from rice
RMATION: (Oryza sativa)"
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Pred. No. 4.5e-08;
0; Mismatches 161;
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NAME/KEY: CDS
LOCATION: Join(1648..4383, 5178..5513)
OTHER INFORMATION: /product- "RRK-F"
OTHER INFORMATION: /note- "Xa21 Xanthomonas spp.
OTHER INFORMATION: resistance gene RRK-F from ric
OTHER INFORMATION: sativa)"
US-08-587-680A-1
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US-08-473-553A-1
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Matches
                                                                                                                                                                             Sequence 1, Application Patent No. 5859338 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bastlan, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pair:
                                                                         APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic
TITLE OF INVENTION: Transformed Plants, and
                                                                                                                                                                                                                                                                                                                      3035
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APPLICATION NUMBER: US 6
FILING DATE: 29-SEP-1995
                  NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach,
                                                                                                                                                                                                                                                                                                                                                                                                   2975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ttcccacttctttgggaaaattgaagtctctggtctttttacggcttaatgacaaccgat 467
                                                                                                                                                                                                                                                                                                                      GCACCAACAATTCAGTGGTTGGATACCA 3063
                                                                                                                                                                                                                                                                                                                                                                                                 TGAGCGGTTCGATCCCATTGGCCATAGGAAATCTTACTGAACTTAATATCTTACTGCTCG 3034
                                                                                                                                                                                                                                                                                                                                                                                                                          tyacggggccaatccctagagcactcactgcaatcccaagccttaaagttgttgatgtct 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCCATCATCGTTGGGCAGGCTTAGAAACTTAGGCATTCTAGTCGCCTACGAAAACAACT 2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGCAATCTTATTGGCTTACAACATCTCTATCTCTGCAACAACAATTTCAGAGGGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                       Application US/08473553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6256 base pairs
  Four Embarcadero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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h, Test, Albritton & Herbert
Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 4.5e-08;
0; Mismatches 161;
                                                                               eic Acids,
and Proteins
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; LOCATION:
US-08-473-553A-1
                                                                                                                                  sequence 15, Application US/08567375
Patent No. 5952485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pairs
                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION UNMER: US/08/473,553A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3120 CTACTACAACAGCTACACCGGTGGTGTTCCACGCGAGTTCGGTGGTTTAACAAAGCTTGA 3179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: S11'A, ROBIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                   3240 GAAACATCTACATACTCTGTTTCTTCACATCAACAACTTAACCGGTCATATACCACCGGA 3299
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3180 GATCCTCGACATGGCGAGCTGTACACTCACCGGAGAGATTCCGACGAGTTTAAGTAACCT 3239
       APPLICANT: Szabo, 'TITLE OF INVENTION:
                                                                                                 APPLICANT:
                                                                                                                                                                                                                                             3360 AATCCCTCAAAGC 3372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                              APPLICANT:
                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                    430 gaagtctctggtctttttacggcttaatgacaaccgattgacggggccaatccctagagc 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 cagcttggatctgtacaacaacaatcttacagggatagttcccacttctttgggaaaatt 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 ctacaaaaacaacatccaaggaactataccttccgaacttggaaatctgaagaatctcat 369
                                                                                                                                                                                                                                                                      550 aatcccaacaaac 562
                                                                                                                                                                                                                                                                                                                                            490 actcactgcaatcccaagccttaaagttgttgtgtgtctcaagcaatgatttgtgtgggaac 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                San Francisco
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Wang, Guo-Liang
Song, Wen-Yuang
Szabo, Veronique
VENTION: Procedures and Materials for Conferring
VENTION: Disease Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                               Ronald, Pamela C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
5117..5467
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2434..5037
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Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 5733;
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FILING DALL.

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/004,645

FILING DATE: 29-SEP-1995

PRIOR APPLICATION WUMBER: US 08/475,891

FILING DATE: 07-JUN-1995

PRIOR APPLICATION NUMBER: US 08/373,375

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; TOPOLOGY: 11:
; MOLECULE TYPE:
US-08-567-375-15
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RESULT
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Best Local Sim
Matches 139;
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REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two
CITY: San I
STATE: Cal:
                                                           273
                                                                                                  495
                                                                                                                                        213
                                                                                                                                                                             435
                                                                                                                                                                                                                     153
                                                                                                                                                                                                                                                            375
                                                                                                                                                                                                                                                                                                                     315 aaaacaaccatccaaggaactataccttccgaacttggaaatctgaagaatctcatcagct 374
                                                                                                                                                                                                                                                                                                                                                                                                       255 ctggacatcttgcgcctgagcttgggaagctttgaacatttacagtatctagagctctaca 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 04-DE
                                                                                                                                                                                                                                                                                              93 GAAATGGTTTCTCAGGTGATATCCCTTCTGATATTGGCAGACTAAAGAGCATCTTAAAGC 152
                                                                                                                                                                                                                                                                                                                                                                               \omega
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                                                                                                                                                                                                             TGGACTCGAGTAGAAACAACTTCTCTGGCACAATCCCTCCTCAGATTGGTAACTGTCTTT 212
                                                       CTCAAATTCACATCTTAAATTACATCAATATTTCCTGGAATCACTT
                                                                                           ctgcaatcccaagccttaaagttgttgatgtctcaagcaatgattt 540
                                                                                                                                                                      ctctggtctttttacggcttaatgacaaccgattgacggggccaatccctagagcactca 494
                                                                                                                                                                                                                                                                                                                                                                             CTGGTGCACTTCCTAGTGCTTTTGGAAACTATTCAGGGCTGAAGAATCTTGTGTTAACTG
                                                                                                                                    CCTTAACTTACTTGGATTTGAGCCAAAAATCAACTTTCTGGTCCTATCCCAGTTCAAATTG
                                                                                                                                                                                                                                                     tggatctgtacaacaacaatcttacagggatagttcccacttctttgggaaaattgaagt 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bastian, Kevin
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ilarity 48.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50.8; DB 4;
Pred. No. 4.4e-07;
0; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    023070-058930
                                                                                                                                                                                                                                                                                                                                                                                                                                                            147;
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US-08-666-271-4

Sequence 4, Application US/08666271 Patent No. 5920000

GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PLANT PATHOGEN RESISTANCE GENES AND USES TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 9326428.1 FILING DATE: 24-DEC-1993 PRIOR APPLICATION DATA: GB 9409363.0 FILING DATE: 11-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/02812
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        2133 TGGACTTCGTACGTTGAACTTGTCTCACAATGTCTTGGAAGGTCATATACCGGCATCATT 2192
                                                                                                                                                                                                                                                                                                2073 TATCAATCTCTCAAAGAACAGATTTGAAGGTCATATTCCAAGCATTATTGGAGATCTTGT 2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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2313 TGTTGGATGCATCCCCAAAGGAAAACAATTTGAT 2346
                                                                                                                                                 2193 TCAAAATTTATCAGTACTCGAATCTTTGGATCTCTCATCTAATAAAATCAGCGGAGAAAT 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      301 totagagototacaaaacaacatocaaggaactatacottocgaacttggaaatctgaa 360
                                 541 gtgtggaacaatcccaacaaacggaccttttgct 574
                                                                                                                                                                                  421 gggaaaattgaagtctctggtctttttacggcttaatgacaaccgattgacggggccaat 480
                                                                                                                                                                                                                                                          361 gaatctcatcagcttggatctgtacaacaacaatcttacagggatagttcccacttcttt 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 19-SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: SADOFF, B.J
                                                                                             | ccctagagcactcactgcaatcccaagccttaaagttgttgatgtctcaagcaatgattt 540
                                                                         22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2880 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    703-816-4100
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HAMMOND-KOSACK, KIM E
THOMAS, COLWYN M
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                         6.18;
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Pred. No. 5.5e-06;
                                                                                                                                                                                                                                                                                                                                                                         Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 2880;
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2913 TATCAATCTCTCAAAGAACAGATTTGAAGGTCATATTCCAAGCATTATTGGAGATCTTGT 2972

361 gaatctcatcagcttggatctgtacaacaacaatcttacagggatagttcccacttcttt 420

301 tctagagctctacaaaaaccaacatccaaggaactataccttccgaacttggaaatctgaa 360

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US-08-666-271-1
                                                                                     ; NAME/KEY:
; LOCATION:
US-08-666-271-1
                                                                                                                                                                                                                                                                                               TELEPAX: 703-815-410 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3905 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 23-DEC-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326428.1

FILING DATE: 24-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9409363.0

FILING DATE: 11-MAY-1994

ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, R.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5920000
Query Match 6.1%;
Best Local Similarity 48.5%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/00
FILING DATE: 19-SEP-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PLANT PATHOGEN RESISTANCE GENES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HAMMOND-KOSACK, I
APPLICANT: THOMAS, COLWYN M
APPLICANT: JONES, DAVID A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: JONES, JONATHAN D
APPLICANT: HAMMOND-KOSACK, KIM
                                                                                                                                          FEATURE:
                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 22201
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                                                                                                                                                          LOCATION:
                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 62
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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898..3489
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SYSTEM: PC-DOS/MS-DOS
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967..3486
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898..966
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Score 48.4; DB 4;
Pred. No. 6.6e-06;
0; Mismatches 141;
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                                  Length 3905;
   Indels
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US-08-244-646-14
                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 1116 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08244646 Patent No. 5744692
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: IT RM 91A 000915
FILING DATE: 06-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/IT/00158
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,064
REGISTRATION NUMBER: 32,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Releace CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: 06-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                         MOLECULE TYPE: DN
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleotide Sequences Coding An TITLE OF INVENTION: Endopolygalacturonase Inhibitor NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3093
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                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                          ORGANISM:
                                                                                                                                                            TOPOLOGY:
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CO
lambda PGIP-3.3
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Albersheim, Peter
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                                                      Phaseolus vulgaris
                                                                                                                                                            linear
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US-08-592-936B-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 48...
Matches 117; Conservative
                                                  TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2917 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/592,936B FILING DATE: 29-JAN-1996 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kellogg, Jill A.
APPLICANT: Bestwick, Richard K.
TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR TITLE OF INVENTION: REGULATED EXPRESSION OF TRANSGENES IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                             REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 caaaaacaaccatccaaggaactataccttccgaacttggaaatctgaagaatctcatcag 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 cttggatctgtacaacaatcattacagggatagttcccacttctttgggaaaattgaa 432
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                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto
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              TYPE: nucleic acid STRANDEDNESS: both
ropology: linear
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Pred. No. 0.00062;
0; Mismatches 126;
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; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: ;
; INDIVIDUAL ISOLATE: ;
; USS-08-592-936B-20
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Search completed: June 23, 2000, 22:45:40 Job time: 40286 sec
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                                                                                                                                                                                                                                                                          Query Match 5.2%; Score 41.4; DB 2; Length 2917; Best Local Similarity 48.1%; Pred. No. 0.0011; Matches 117; Conservative 0; Mismatches 126; Indels 0;
                                                                                             313 CABABACBACRATCCBAGGARCTATACCCTCGCCAACCTCGCCAACTCAAACTCACCAACTCCACTA 1766
                                                                                                                                        1947 CCC 1949
                                                                           553 ccc 555
                                                                                                                                                                                                                                                                                                                                         sequence of the drul:PGIP chimeric gene
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Title:
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Listing first 45
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  length: 0
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Gapop 10.0 , Gapext 1.0
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em_est8:*
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46: 9b_est26:*

48: 9b_est29:*

48: 9b_est39:*

50: 9b_est31:*

51: 9b_est31:*

52: em_est21:*

53: em_est21:*

55: em_est22:*

56: em_est23:*

58: em_est23:*

61: 9b_est33:*

61: 9b_est33:*

61: 9b_est44:*

62: 9b_est44:*

63: 9b_est43:*

64: 9b_est43:*

65: em_est29:*

66: em_est29:*

67: em_est29:*

68: em_est29:*

70: 9b_est41:*

71: 9b_est41:*

72: 9b_est42:*

73: 9b_est43:*

74: 9b_est43:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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R89998 556 bp mRNA EST 30-DEC-1997 TION 16333 Lambda-PRL2 Arabidopsis thaliana cDNA clone 187H5T7, mRNA sequence. TION R89998.1 GI:957538 EST. Thale cress. Arabidopsis thaliana characophyta; Embryophyta; Tracheophyta; thale cress. Arabidopsis Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudhortylcophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCE 1 (bases 1 to 556) I (bases 1 to 556) Newman, T. deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones NAAL Plant Physiol. 106, 1241-1255 (1994)	280 35.5 695 64 AW038168 AW038168 EST279825 278.6 35.3 305 25 N65416 278.6 35.3 305 25 N65416 278.6 35.3 305 25 N65416 278.6 35.3 305 25 N65416 278.6 35.3 305 25 N65416 278.6 35.3 305 25 N65416 278.6 35.3 305 25 N65416 278.6 35.3 305 25 N65416 278.6 35.3 305 25 N65416 278.6 35.3 305 25 N601134 278.6 35.3 305 25 N601134 278.6 35.3 305 26 AW319797 278.4 33.6 637 80 AW320075 281.4 33.1 676 74 AW220075 281.4 33.1 676 74 AW220075 281.4 33.1 545 44 AW307836 257.6 31.2 545 44 AW307836 258.2 30.7 52.2 46 AW307836 258.2 30.7 52.2 46 AW3037836 259.8 541 64 AW0318587 231.4 28.9 336 20 334187 232.6 29.8 541 64 AW034682 232.8 29.5 612 47 AM496325 232.6 28.5 515 79 AW279515 232.6 28.5 515 79 AW279515 232.6 28.2 568 47 AM27370 231.4 28.1 516 42 AW033591 231.2 27.7 497 59 AM772079 2318.2 27.7 497 59 AM772079 2318.2 27.7 497 59 AM772079 2318.2 27.7 498 240 54 AW033591 231.6 26.7 46.3 74 AW321200 231.6 26.7 46.3 74 AW331917 230.6 26.6 442 42 AM031917 230.6 26.6 442 AM321200 240.8 24.9 360 42 AM100481 250.8 24.9 360 42 AM100481 250.8 24.9 360 42 AM100685 250.6 24.9 360 42 AM100685 250.6 24.9 360 42 AM100685 250.6 AM32100685 250.6	Match Length DB ID 556 23 R89998 46.7 469 63 A1992868 44.3 364 42 A1100682 41.5 353 23 H37300 41.4 534 33 AA394359 40.3 720 64 AW03110 39.9 339 42 A1100679 38.8 401 37 AA712221 38.8 401 37 AA712221 38.2 336 23 H37396 38.2 336 23 H37396 38.2 336 23 H37396 38.3 36 23 H37396 37.6 511 74 AW221278 37.6 511 74 AW231278 37.6 511 74 AW231088
Qy 491 ctcactgcaatcccaagccttaaagttgttgatgtctcaagcaatgatttgtgtggaaca 550	/note-"vector: lambda Zip-Lox; Site_1: Sal; Site_2 Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources we day germinated etiolated seedlings; 2) tissue cult grown roots; 3) staged plants half with 24 hour library derived from equal cycle, half on 16 hr light, 8 hour dark-rosettes; same plants as 3 but aerial tissue (stems, flowers siliques. The vector is BRL's lambda Zip-Lox. The inserts were directionally cloned with Sal-Not arm oligo dT primed cDNA. " SE COUNT 151 a 118 c 123 g 146 t 18 others IGIN 50.1%; Score 395.4; DB 23; Length 556; Best Local Similarity 94.4%; Pred. No. 1.1e-98; Matches 441; Conservative 0; Mismatches 20; Indels 6; Ga 251 ctctctggacatcttggggccttggggaagcttggaagcttggaactttgaagcatctgaagctccllid	MEDLINE 95148729 COMMENT On Apr 14, 1993 this sequence version replaced g1:693023. Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, Mi Tel: 517-353-9168 Email: 22313tcneibm.cl.msu.edu Seq primer: T7 dye primer. FEATURES 1556 1556 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /clone="18715T7" /clone="18715T7"

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

RESULT 1
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DEFINITION

CDNA

clone

21-AUG-1998 187#5XP 3',

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On Dec 20, 1
Contact: Dav
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Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-27-3324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carplo, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Roseiga, A., Murry, L., Turner, C., Krikorlan, S., Elder, L. and Warron, A., Murry, L., Turner, C., Krikorlan, S., Elder, L. and
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On Dec 20, 1995 this sequence version replaced
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Location/Qualifiers
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Arabidopsis thaliana Ohio State clone set."
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2.7e-91;
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aactttgagaacaacccgaggttggagggaccggaattactcggtcttgcaagctacgac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: 22313tcn@ibm.cl.msu.edu
The sequence entry for this EST has
Is being submitted in the sense orie
Seq primer: M13-21.
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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, Retzel, E. and Somerville, C.
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Tel: 517-353-0854
Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On May 5, 1995 this sequence version replaced Contact: Thomas Newman MSU-DOE Plant Research Laboratory
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33804 Lambda-PRL2 Arabidopsis thaliana
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MSU-DOE-PRL, Michigan State University, Plant
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/clone="115"/Lambda-PRL2"
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/clone="115"/Lambda Zip-Lox: Site_1: Sal; Site_2: Not;
/note="vector: lambda Zip-Lox: Site_1: Sal; Site_2: Not;
/note="vector: lambda Zip-Lox: Fine mrNA sources were 1) 7
guantities of 4 pools of mRNA. The mrNA sources were 1) 7
day germinated etiolated seedlings: 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo df primed cDNA.

13 a 80 c 70 g 99 t 2 others
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/strain="var columbia"
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1 (bases 1 to 348)

1 (bases 1 to 348)

Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,

Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

Plant Physiol. 106, 1241-1255 (1994)
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On May 5, 1995 this sequence version Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University
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The sequence entry for this EST
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/clone="185L1XP"
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/strain="var columbia"
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Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Tel: 517-353-0854
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                                                                                                                                                                                                                                                                 ll: 22313tcn@ibm.cl.msu.edu
primer: T7 dye primer.
              /note-Tyector: lambda Zip-Lox; Site_1: Sal; Site_2: Not Lambda PRI2 is a CDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sourcess were day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and
                                                                                                                                                           /organism="Arabidopsis
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/clone="179J19T7"
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                                                                                                                                                 Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.

Retzel,E. and Somerville,C.

Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)

95148799

On May 18, 1995 this sequence version replaced gi:811121.

Contact: Thomas Newman
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.

MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                       Arabhidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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25942 Lambda-PRL2
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AA394359.1 GI:2047570
                                                                                                                                                                                                                                                                                                                            Arabidopsis.

1 (bases 1 to 534)
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                                                                                                22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. " a 85 c 67 g 89 t 14 others
/organism="Arabidopsis
/strain="var columbia"
/db_xref="taxon:3702"
/clone="305G1T7"
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.5%;
94.1%;
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Arabidopsis thaliana
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Pred. No. 4.6e-80;
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                                          thaliana"
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cDNA clone
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305G1T7 3',
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REFERENCE
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VERSION
KEYWORDS
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ORGANISM
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AW443205
LOCUS
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Best Local Sim
Matches 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAA
Lycopersicon.

1 (bases 1 to 608)

1 (bases 1, to 608)

D'Ascenzo, M., He,X., Lyman,J., Matern,A.L., Vision,T.,
Liang,F., Hansen,T.S., Ronning,C.M., Craven,M.B., Bowman Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Giovannoni,J.J. and Martin,G.B.
Generation of ESTs from tomato callus (mixed elicitor)
                                                                                                                                        Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                AW443205 608 bp mrNA
EST308135 tomato mixed elicitor, I
clone cLET43M10 5', mrNA sequence
aw443205
                                                                                                                                                                                                                                                          EST
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/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA.

51 a 114 c 125 g 126 t 18 others
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Pred. No. 8.1e-80;
0; Mismatches 45;
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                                                                Bowman, C.L.,
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                                                                                    Holt, I.E.,
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Best Local Similarity
Matches 401; Conserv
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                                                                                  atcccaagccttaaagttgttgatgtctcaagcaatgatttgtgtggaacaatcccaaca 559
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                                                                                                                                                                                                                                                                                                                                                                                                                      acctgtaaccaagacaaccgcgtcactcgtgtggatttggggaattcaaacctctctgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAAAGGGGAATTCAGAAGGGGATGCTTTGTACGCCCTCCGCCGGAGCTTATCTGACCCG
                                                                                                                                                                                                CTGTACAACAACAATATTTCGGGGACAATTCCTACTTCACTTGGAAAACCTGAAAAACCTT
                                                                                                                                                                                                                                                                                                                    aacatccaaggaactataccttccgaacttggaaatctgaagaatctcatcagcttggat 379
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                                                                    TCTGGTCCATTTGAGCATATTCCTCTAAACAATTTCGAGCACAATCCTCGACTTGAAGG
                                                                                                                                                                                 GTTTTCTTGCGTCTAAATGATAACAAGCTAACAGGACCAATCCCAAGAGAACTTACTAGC 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Dec 20, 1995 this sequence version Contact: David Frisch Clemson University Genomics Institute Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 Jordan Hall,
 AW031110
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864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF',"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2
Xho1; cLET - Inoculated with a variety of disease respo elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. Eco site was destroyed during cloning."

a 126 c 134 g 183 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="cLET43M10"
/clone_lib="tomato mixed elicitor,
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
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Pred. No. 2.2e-77;
 mRNA
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JOURNAL
COMMENT
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AUTHORS
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ORGANISM
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VERSION
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 ctgtacaacaactcttacagggatagttcccacttctttgggaaaattgaagtctctg
                                                                                                catcttgcgcctgagcttgggaagcttgaacatttacagtatctagagctctacaaaaac
                                                                                                                                                       acctgtaaccaagacaaccgcgtcactcgtgtggatttggggaattcaaaacctctctgga
                                            aacatccaaggaactataccttccgaacttggaaatctgaagaatctcatcagcttggat
                                                                                   CATTTGGTACCTGAGCTCGGAAAGCTTGAACATCTACAGTATCTGGAGCTTTACAAAAAT
                                                                                                                                         ACTTGCAACGGAGATAATCAAGTTACTCGTGTGGATCTTGGGAACTCAAAGTTATCTGGT
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AW031110.1
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/clone="clEC13C21"
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/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="callus"
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74.3%;
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Pred. No. 4.2e-77;
0; Mismatches 138;
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Gaps

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482 379 422 319 362 259

720; 0

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DEFINITION
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cLEC13C21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute Clemson University
/note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; supplier: Giovannon1 laborator; CLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library" 149 c 143 g 228 t
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                                                                                                                                                                                                                                              /dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="tomato callus,
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33800 Lan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: 22313tcn@ibm.cl.msu.edu
The sequence entry for this EST has been reverse
is being submitted in the sense orientation.
Seq primer: M13-21.
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Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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517-353-9168
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Lambda-PRL2
                                                                                                                                                                                                          Inote="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is RLL's lambda Zip-Lox. The CDNA the content of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of the colon of
                                                                                                                                inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. "
75 c 66 g 89 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis
/strain="var columbia"
/db_xref="taxon:3702"
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/clone_lib="Lambda-PRL2"
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Arabidopsis thaliana
Score 314.6; DB Pred. No. 2e-76;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
euphyllophytes; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on Sep 19, 1997 this sequence version replaced gi:1520373. Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University Michigan State University Plant Biology Bldg., E. MSU-DOE-PRL, Michigan State University.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA cplant Physiol. 106, 1241-1255 (1994)
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Tel: 517-353-0854
Fax: 517-353-9168
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primer: T7 dye primer.
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/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: No
/note="Vector: lambda Zip-Lox; Site_1 Sal; Site_2: No
Lambda PRL2 is a CDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
                                                                                                                                                                                                              /db_xref="taxon:3702"
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,S., Thomashow,
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Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
plant Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
H37296
                                                                                                Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
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                                                                                                                                               On May 8, 1995 this sequence version
                                                          Lansing,Mi
Tel: 517-353-0854
                                                                                     MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E
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           : 517-353-0854
: 517-353-9168
!1: 22313tcn@ibm.cl.msu.edu
primer: T7 dye primer.
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a 105 c 78 g 99 t 16 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGTCGAAGCAAACTCCGAAGGAGTNGCTCTTTACGCTCTTCGCCGGAGTTTAACAGAT
                            Generation of ESTs from Unpublished (1999) On Jul 8, 1999 this sequent Contact: David Frisch
                                                                                                                                                                      1 (bases 1 to 646)
Alcala,J., Vrebalov,J., White,R., Matern,A.L.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksle
                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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University
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Pred. No. 8.6e-
0; Mismatches
                                                                                                                    tomato
                                                        version replaced
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Tanksley,S.D.
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Ahn, S.,
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376;
                                                                                                                                 aacggaccttttgctcacatt 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATTTGGTACCTGAGCTCGGAAAGCTTGAACATCTACAGTATCTGGAGCTTTACAAAAAT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catcttgcgcctgagcttgggaagcttgaacatttacagtatctagagcttctacaaaaac 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acctgtaaccaagacaaccgcgtcactcgtgtggatttggggaattcaaacctctctgga 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAAAGGGGAATTCAGAAGGGGATGCTTTGTACGCCCTCCGCCGGAGCTTATCTGACCCG 205
                                                                                                                                                                                                  atcccaagccttaaagttgttgatgtctcaagcaatgatttgtgtggaacaatcccaaca 559
                                                                                                                                                                                                                                                   GTTTTCTTGCGTCTAAATGATAACAAGCTAACAGGACCAATCCCAAGAGAACTTACTAGC 565
                                                                                                                                                                                                                                                                        CTGTACAACAACAATATTTCGGGGACAATTCCTACTTCACTTGGAAACCTGAAAAACCTT 505
                                                                                                                                                                                                                                                                                                                                                                                            AATATTCAGGGAACCATCCCTAAGGAGCTCGGTAACTTGAAGAGCCTTATTAGTCTGGAT 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTAACGTGTTACAGAGCTGGGATCCAAATCTTGTTAACCCTTGTACCTGGTTTCATGTC 265
                                                                                                                                                                             ATTTCTAGCCTGAAAGTTGTGGATGTCTCGAATAATGATTTGTGTGGAACAATTCCTACT 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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100 Jordan Hall, Clemson,
Tel: 864 656 4366
   AW350720
GM210009A10F4R
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/dev_stage="red ripe (7-20 days post-breaker)"
/dev_stage="red ripe (7-20 days post-breaker)"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
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post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
81 a 126 c 138 g 201 t
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   657 bp
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Glycine max
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1.2e-72;
   CDNA
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KEYWORDS
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AUTHORS
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VERSION
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JOURNAL
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                                   236 ttggggaattcaaaacctctctggacatcttgcgcctgagcttgggaagcttgaacattta 295
                                                                                                                                                 176 aatoottgtacotggttccatgtcacotgtaaccaagacaaccgcgtcactcgtgtgtggat 235
                                                                                                                    AGTCCCTGTACNNNNNTCCACGTCNNNNGCAANCAGGACANNNNNGTCACTCGAGTGNAT 598
NNTGGTAACTCTAACCTATCTGGACATTTGGTACNNGAACTTGGGAAGCTGGAGCATCTA
                                                                                                                                                                                                                                        al Similarity 73.0
363; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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On Nov 22, 1999 this sequence version replaced g1:6462107.

Contact: Vockin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)

Lewin, H. A., Director, Keck Center for Comparative and Functional
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Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 572-322 FAX:(888)919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome ystems.com web site:www.genomesystems.com seg primer: 5'-TTTTTTTTTTTTTTTTTTTTTAA/C/G)-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW350720
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Fax: (217) 333-4582
Email: 1-vodkin@uiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Edwin R. Madigan
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                                                                                                                                                                                                                                                                                                                                                                                                                            190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; Library Gm-r1021 is a sequence-driven, reracked set
of the original library Gm-c1004 which was prepared from
root cDNA. The mRNA was isolated from entire roots of 8
day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize
the cDNA. The Gm-c1004 library was constructed by Dr.
Paul Keim & Virginia H. Coryell, Department of Biology,
Box5640, Northern Arizona University, Flagstaff, Az
86011, email: paul.keimenau.edu, virginia.coryell@nau.edu.
The contig analysis to select unique genes was performed
by the laboratory of Ernest Retzel, Computational Biology
Centers University of Minnesotte.
                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.life.uiuc.edu/biotech/keck.html."
131 c 120 g 191 t 25 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.genomesystems.com, and seq
Center for Comparative and Functional
University of Illinois,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Centers, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
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/clone_lib="Gm-r1021"
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AW221278 AW221278.1 GI:6532962
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                                                                                                                                                                                                                                                                    Generation of ESTs from tomato fruit tissue Unpublished (1999) On Jul 7, 1999 this sequence version replace Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                      Clemson University Genomics Institute
                                                                                                                                                                                     Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                        Clemson University
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                                    /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/db_xref="taxon:4081"
/clone="cLEF13N13"
/clone_lib="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/tissue_type="fruit pericarp"
/tissue_type="fruit pericarp"
/tissue_type="fruit pericarp"
/lab_host="SOLR"
/note-"Vector: pBlueScript SK(\); Site_1: EcoR1; Site_2: Xhol; cLEF - Fruit were tagged at the 1cm stage and harvested 3-5 days prior to ripening. Fruit were cut in
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CLEC21C20, mRNA seque
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                               Unpublished (1999)
On Dec 20, 1995 this s
Contact: David Frisch
                                                                                                               Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
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                                                                                                                                                                                                                                                                                                                              380 ctgtacaaccaatcttacagggatagttcccacttctttgggaaaattgaagtctctg 439
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                                                                                                                                         CTTTTCTTGCGTCTAAATGATAACAAGCTAACAGGACCAATCCCAAGAGAACTTACTAGC 653
                                                                                                                                                                                CTGTACAACAACAATATTTCGGGGGACAATTCCTACTTCACTTGGAAAACCTGAAAAACCTT 593
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ATTTCTAGCCTGAAAGTTGTGGATGTCTCGAATAATGATTTGTGTGGAACAATTCCTAC
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Search completed: June 23, Job time: 27431 sec 2000, 19:06:38

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(without alignments)
-69.776 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result O a a Ω ი 894 361 361 356.2 330 119.4 106 95.4 Score 63.4 63.4 63.63 Query Match 9 4604 9 2089 7 18155 7 18756 8 43277 8 43277 8 43277 8 43277 9 84718 9 98471 9 98471 9 98475 9 111945 7 111945 6 8151 9 6475 6 8151 8 108355 5 108355 6 8151 8 6471 4 183649 4 197254 4 197254 4 197254 4 197254 1 175053 3 2 94362 2 127053 2 127053 2 127053 3 114935 2 177161 3 15936 3 15936 3 114935 1 114935 1 114935 1 114935 Length BB AB029327 AB010698 E12705 AB010698 E12705 AC701275 AC012654 AC002334 SBU62279 AC021198 AC005957 AC005287 A57133 U42445 A57130 T1N24 AC006532 ATT16K5 ATT9C5 AC007651 A67432 DCU93048 A67797 A67823 A67821 A67825 A67819 A67817 AC005395 AC008017 ATF18F4 LELRPGENE A67827 AF053994 X95269 L. esculentu A67827 Sequence 32 U93048 Daucus cars A67827 Sequence 2 U622797 Sorghum bic AL049917 Arabidops AB010698 Arabidops E12705 Arabidops E12705 Arabidops E12705 Arabidops E12705 Arabidops E12705 Arabidops AC011524 Arabidops AC0115254 Arabidops AC0115254 Arabidops AC011527 Arabidops AC011527 Arabidops AC011527 Arabidops AC011527 Arabidops AC0115287 Arabidops AC015287 Arabidops AC015395 Arabidops AC015397 Lycopersi A67823 Sequence 28 A67821 Sequence 26 A67825 Sequence 30 A67819 Sequence 24 A67817 Sequence 22 Description A67796 Sequence A67428 Sequence

ALIGNMENTS

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Sequence :
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De, V.S., Schmidt, E.D., Van, H.G. a
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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LTGPIPRELTVISSLKVVDVSGNDLCGTIPVEGPFEHIPMQNFENNLRLEGPELLGLA
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Best Local Similarity 72.4
Matches 538; Conservative
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De, V.S., Schmidt, E.D., Van, H.G. a
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
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/prottein_id="CAB42248.1"
/db_xref="GG:4756644"
/translation="retrrenveneleaasilitialihiveansegdalyalersit /translation="retrrenveneleaasilitialihiveansegdalyalersit /translation="retrrenveneleaasilitialihiveasilselityenningenelegdalyalersiteiloyile iyknniogilseselgalkalisildinningenelegdeligiasydin /retrrenvenelegdeligiasydin /retrrenvenelegdeligias
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Sequence 30 from Pates
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A67825.1 GI:4756647
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De, V.S., Schmidt, E.D., Van, H.G. and
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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  313
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                                                                                          'note="unnamed protein product"
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De, V.S., Schmidt, E.D., V

PRODUCTION OF APOMICTIC
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Pred. No. 6.7e-73;
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ALTAIPSLKYYDYSSNDLCGTIPTNGPFAHIPLQNFENNPRLEGPELLGLASYDTNCT
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/note="unnamed protein product"
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                    gggaaaattgaagtcacttgtttttttgcggcttaacgaaaaccgattgaccggtcctat 494
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           GGGAAAATTGAAGTCTCTGGTCTTTTTACGGCTTAATGACAACCGATTGACCGGTCC-AA
                                                    GAATCTCATCAGCTTGGATCTGTACAACAACAATCTTACAGGGATAGTTCCCACTTTCTT
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De, V.S., Schmidt, E.D., Van, H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 974347-8 20-NOV-1997; CIBA GEIGY AG (CH)
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2 (bases 1 to 4604)

Tornero, P., Mayda, E., Gomez, M.D., Canas, L., Conejero, V. and Vera, P. Characterization of IRP, a leucine-rich repeat (LRR) protein from tomato plants that is processed during pathogenesis
Plant J. 10 (2), 315-330 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
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1 (bases 1 to 4604)
                               346. .2380
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           thale cress.
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Eukaryota; Viridiplantae; Streptophyta; endicotyledons; core
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eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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V.S., Schmidt, E.D.
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WIQSWOPTIVNFCTWFHYTCHNENSVIRVDLONAELSGHIVPELGYLKNLQYIELYS
NNITGFIPSNLGNIRLVSLDIYLNSFSGPIPSELGYLKNELGYIENLYSLIPS
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195. .2072
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                                               embryogenesis receptor-like
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Schmidt, E.D., Guzzo, F., Toonen, M.A. and de Vries, S.C. A leucine-rich repeat containing receptor-like kinase marks somatic plant cells competent to form embryos Development 124 (10), 2049-2062 (1997)
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Submitted (12-MAR-1997) Molecular Biology, Agricultural University
of Wageningen, Dreyenlaan 3, Wageningen 6703 HA, The Netherlands
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Schmidt, E.D.L., Guzz
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
1 (bases 1 to 1815)
De,V.S., Schmidt, E.D., Van,H.G. and Hecht,V.F.
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
                                      SBU62279 936 bp mRNA PLN 09-DEC-1996 Sorghum bicolor leucine-rich repeat-containing extracellular glycoprotein mRNA, complete cds. U62279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctccgaaggggacgctcttcacgcgctttcgccggagcttatcagatccagaccaatgttgt 74
                                                                                          ---GGATCTCTGGGACAACCTTCTTACCGGCGAAATCCCAACTACGCTTGGTTCTGTCAG
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                                                                                                                                tagtgaactctacaaaaacgagattcaaggaactataccttctgagcttggaaatctgaa
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                                                                                                                                                                                                                                                                        tgattatctgaaaacatttacattatcagtcacacatataacattttgctttgagtcata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol.
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(bases 1 to 936)
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/db_xref="GI:1710124"
/db_xref="GI:1710124"
/translation="Mapcfaaagfligilalatfascntegdilykorlawedpunvl
/translation="Mapcfaaagfligilalatfascntegdilykorlawedpunvl
oswnstlanpctwfhvtcnunpvlrvdlgnagisgpllpdlaeignlgytelygngl
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/note="leucine-rich repeat-containing extracellular
glycoprotein; contains six N-glycosylation sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/db_xref="taxon:4558"
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GAAGCATTACCACGCTAAAGGTTCTTGATTTCTCCGATAATGCGTTAACCGGCGAGATTC
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Arabidopsis thaliana
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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1 (bases 1 to 43277)

Lennard, N., Quail, M., Harris, B., Rajandream, M.A. and Barrell, B. Direct Submission

Submitted (20-MAY-1999) EU Arabidopsis sequencing project, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge Sanger Centre, Wellcome Trust Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For more information about this sequence or the ESSAII project, see MIPS http://websvr.mips.biochem.mpg.de/proj/thal/. Order of segments is not known; 800 n's separate segments.

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence.

* as soon as it is available and the accession number will
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/variety="Columbia"
/db_xref="taxon:3702"
/clone="15F17"
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T5F17, *** SEQUENCING IN PROGRESS
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                                   950 TGTATACTAACTTTCTTAATGGTTCTATTCCTATTTCATTGGGGAATTTGACGAGCTTGT 1009
                                                                                    323 totacaaaaacgagattcaaggaactataccttctgagcttggaaatctgaagagtctaa 382
                                                                                                                                                                                          Match 8.7%; Local Similarity 57.0%; local Similarity 57.0%; les 142; Conservative
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Isolation of the gene for EIR, an elicitor-inducible receptor-like protein, from tobacco by Differential Display Unpublished (1999)
2 (bases 1 to 2786)
Takemoto,D. and Kawakita,K.
Direct Submission
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Location/Qualifiers
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SLSSISLYENHLSGPIPSSLGNLLDLYVLYLYLANQLSGPIPSSLGNLKNLNYKKLHON
QLNGSIPASFGNLRNMQYLFLBSNNLTGEIPLSICNLKSLKYLSLGRNSLKGDILQCL
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NTVSTLDDQESTSEFLNDFWKAALMGYGSGLCIGLSILYFMISTGKLKWLSRITEWLQ
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/db_xref="taxon:4097"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://www.dna.affrc.go.jp:82/, Tel:81-298-38-7441, Fax:81-298-38-7468)
The orientation of the sequence is from T7 to SP6 of the PAC clone. Genes were predicted from the integrated results of the following:GENSCANI.0, BLASTNZ.0, BLASTNZ.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against the non-redundant database NRP (PIR, SWISSPROT, GENPEPP, PDB) from MAFF DNA bank and the cDNA sequence database at RGP. Protein similarities of the cording regions were searched against NRP with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession
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Sasski, T., Matsumoto, T. and Yamamoto, K. Direct Submission
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Oryza sativa
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Detailed information on assemble quality together with annotation of this entry at http://www.dna.affrc.go.jp:82/genomicdata/GenomeFi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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/db_xref="taxon:4530"
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/clone="p0003H10"
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BAC clone F22K18 (AL035356)"
                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa"
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PESCGGGDEEGVAGDVTTPSAEWVTAASPHLRLPRSKDVVVNGCVVKVKYCDTCLLYR
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                                                                                                                                                                   thaliana DNA chromosome
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/translation="medygfeysddepeeqdydiengyynskgmyetdbegalagfdq
/translation="medygfeysddepeeqdydiengyynskgmyetdbegalagfdq
/transpekaemgfralkgotkilyklokkemadayremltylksavtrnysbekolnn
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Ilkelhkscqredgsddokkgtqllevyaieiqmyetknnkklkelytkalsiksal
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Mesevnpfdggeakpykndpeilamtnliaatgkndimeikilksnrtiinddpfir
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NYIEDLLKNIKTQVLLKLIKPYRTIRIFFISQKMCMKIISNMEIMYILVJEHGTLVYI
RAILGSCKKYSLKIDLFLSCAQTRYQLKSCALMRADPMLETEMYLLSYSVDDALSSI
VLSMFCMELMFPEKDVEGOLVSILIDNRIGGHIDQVMKLERGDREIPSHRQVEYSAE
EHLDNGVQSWYBEIAGCIGCTALGTCHVLLMMMLGFCPELMISANSNPSETILASM
ANNEMECMHCRESKFWSGRENWERKYKAPGTHTANIVPLESSDVANGSLSNQNEG
ANNEMECMHCRESKFWSGRENWERKYKAPGTHTANIVPLESSDVANGSLSNQNEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"ESTS D47452(S12946),C23573(S10086),C19173(E10057), AU081294(E10057),AU032455(S10086) correspond to a region of the predicted gene.; Similar to PNIL34. (U37437)"
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/db_xref="G1:6498423"
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RQMRRGAPPDDASPCDLATIGVGRRWKKWDAEEGVGVAEEEERMAAGRARQLRGE
GGGVVVAHKRRSGAREEERRGGGFERRSGGDERGGVEEEDKAEPVGRRENKGERIGE
TDERRMPGHSHKPSIILMWIQTTKPARRRGANVLARHCGDDRRRRCRSQCAVARRRQE
ALPIGSLFPYLYEMIRDLKVNAKEEQDLGFYAGFVAGCTVQAYASEVCRKEHQALGISL
VTSSRAIALVVGPALGGFLGGETLHHHHDDKEVIDALEADDATSDLGETTKEGSGSRU
VTSSRAIALVVGPALGGFLGGETLHHHDDKEVIDALEADDATSDLGETTKEGGSGSRU
GHTKSLLKNWQLMSAITLYCVFSLHDTAYLEIFSLMAVSSRKYRGLSFTSQDVGIVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(13373 .13457,15836 .15914,17237 .17477,17560 .1
17726 .17860,18400 .18587,18681 .18749,18826 .18916,
19028 .19162,19323 .19379,19349 .19441,19450 .19509,
19523 .19585,19589 .19701,19800 .19941,20057 .20294,
21399 .21586)
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DVENPEFKRKLDRMVEINKKIIAIGESDDIPLVKNLKRIPHVAALVSEIIAAYLMPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAAKPGTPKKRGKTEIQETLLTPRFYTTDEDEMERLFNAEINKQLNQEEFDALLQEFK
TDYNQTHFYRNPEFKAAADKMEGPLRQIFVEFLERSCTAEFSGFLLYKELGRRLKKTN
PVVAEIFSLMSRDEARHAGFLNKGLSDFNLALDLGFLTKAKKYTFFKPKFIFYATYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHNEDCESTPTAVSHHVNSERL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYDKKENPYNRGAISNIAEVFCAGIPPSMNNFRSWVAPPPLEEPDDVSGQLPPRNGAD
LTGGVKEKVDLEMGRNGGIIPAILRGLDYDEMEKNDVSVHIKDRGAAPAAPDPFMAGR
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VAHKDGNDGSLLKSMAGEPLSVVLIVYTFVSVWFVGGLTVFHLYLMSTNQTTYENFRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAELRHVMTNLGEKLIDEEVEEMIREADVDGDGQINYDEFVKVMMAK"

complement(join(24778. 24897,25615. 25722,25808. 25893,

26090. 26177,26435. 26638,27519. 27581,27708. 27778,

28329. 28389,28512. 28552,29058. 29225,30476. 31136))

/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(22475 . 22550,23332 . 23705)
/notbe="ESTS AUG30013(E50493), AUG81341(E50493) correspond
to a region of the predicted gene.; Similar to O.sativa
gene encoding calmodulin. (Z12828)"
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/db_xref="GI:6498420"
/translation="MASSAMELSLLNPAAMRGLSAAKPRVVSSRRIVRFRVASSAAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the predicted gene.; Similar to /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KESPFLSYTTDQQALNLQREHTTLSDNVINLSEGSYRPLAPSSHLGHPVYTIFYVDDN
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TEAELQDMINEVDADGNGTIDFPEFLNLMARKMKDTDSEEELKEAFRVFDKDQNGFIS
ISGFGYLVYQLAIYPLLAKYYGPIKPFRYAAVLSILLLSTYPFMANLYGLELKYLINI
ASLLKNMFANKKEMTNQSISLLDAGFHGRKSTLLGCSYQVKQQGSSKP"
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/db_xref="GI:6498422"
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join (40347. 40358, 40468. 40680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MSRGRGRAPATACGSVRCYABEVAPEQEDSARVALLLIRLRDSP ARTAPPKLARRIRDHGVPLLERDEDLISVGPTLD"
join(48412. 48822,49072. 49179,49283. 49438,49876. .5009 50202. .50411,50488. .50625,50842. .50943,51105. .51170, 51274. .511551, 51551, 7005e="Similar to Arabidopsis thaliana chromosome II BAC 777A15 sequence; hypothetical protein. (AC005496)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mhpknhivaaarvilvlosplpsssfsnrrrrrqcrpTiaiaT
ADGSTREVLpppDRGGKGGFRRMRMKEGGD"
complement(join(42025 . 42083,43481 . 43661))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(52616. .52685,53228. .53299,53395. .53466,53657. .53800,54663. .54734,56026. .56334))
/note="ESTS C97644(C60871),AU081265(C60871) correspond to a region of the predicted gene.; Similar to Lesculentum LRP gene. (X95269)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAA87827.1"
/db_xref="GI:6498424"
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                                                                                                                                                                                                                                                                                                                                              /translation="MAAAWSPALAAVLLAAAVASASNSEGDALYALRRALADPRGVLQ
SWDPTLVNPCTWFHVTCDRAGRVTRLDLGNSNLSGHLAPELGHLEHLQYLELYKNNIQ
GTIPAELGSLKNLISLDLYNNNITGTIPKELGKLSSLVFLRLNDNSLNGPIPRDLAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFSQSGLYSNHQDIGPRYAGVLLGLSNTAGVLAGVFGTAATGYILQHGSWDDVFKVSV
VLYLVGTLVWNLFSTGEKIID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSVFYSFGSLGVFWFSTWASKAYSSPLEDPGISAEEKKLITSQTTGGEPVKEIPWGLI
LSKPPVWALIVSHFCHNWGTFILLTWMPTYYNQVLKFNLTESGLFCVLFWLTMAVSAN
FGGWIADTLVSRGLSVTTVRKIMQSIGFLGPAFFLTQLSHIDSPAMAVLCMACSQGTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRALRGTDVRSNTSSSSSRKGRHDDARHDGGYGDDGDAGALLASVRRLLLSGSAQDD
AAEGEAEEDEQGQFFKRWAIVFLCFSAFLLCNMDRVNMSIAILPMSAEFGWNPQTVGL
IQSSFFWGYLLTQIAGGIWADTVGGKTVLGFGVIWWSIATALTPFAAKLGLPFLLVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MAAGDKAGGDDAAAAAPLLVPAAAGRRRRCPGCRTKERCEAHPG
| PYLNPYLTYMIVCICASAVNRVEATEVMPTSTSVS"
|Join(47081: .47084.47194. .47313.47469. .47584)
/note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                            SSLKVIDVSNNDLCGTIPTSGPFEHIPLNNFDKNPRLEGPELQGLATYDTNC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFMGVGEGVAMPAMNNILSKWVPVSERSRSLALVYSGMYLGSVTGLAFSPLLIHNFGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="BAA87830.1"
/db_xref="GI:6498427"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAA87829.1"
/db_xref="GI:6498426"
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/db_xref="GI:6498425"
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                  /translation="mrrsrartdlraagrataelrrrgrrsrgrgqeeylgtaslggg
EGSTSDEWEGRGGEGRGGAAAVRPAGEERRRHRAETKLGLSILVGGRGAPHRQSGGHG
                                                                                                                                                 KTGTSSLTGSVPSKDRSRNRPGVNLADH" complement(join(63689. .63842,63844.
                                                                                                                                                                                                                   /protein_id="BAA87833.1"
/db_xref="GI:6498430"
                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAA87832.1"
/db_xref="GI:6498429"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAA87831.1"
/db_xref="GI:6498428"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start
                                                                                                                                                                                                                                                                                   /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MLYLLPLSVSCRVPGSPPAPRSRRFLDPGGGRGVGDGLGGVRVF"
eggrdeegelmlyggalrpeeeeeeghgrrrgrrgeerrrycerereer"
                                                           /protein_id="BAA87834.1"
/db_xref="GI:6498431"
                                                                                                                          /note="hypothetical protein"
                                                                                                                                                                                            /translation="MKLLKVDHPRSHHTVFLYASLTSIALYTSLTIIVEKTGLAVQPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ld="BAA87828.1"
                                                                                                                                                   .64145))
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/chromosome="5"
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55.7%;
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                                                                                                                                                                                                                                                      323 totacaaaaacgagattcaaggaactataccttotgagottggaaatotgaagagtotaa 382
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                                                                                                                            tcagtttggatctgtacaaccaatctcaccgggaaaatccccatcttctttgggaaaat 442
                                                                                                                                                                                                        TGTATTCAAATGATCTTGAAGGTCCAATTCCTGAAGAAATGTTTGATATGAAGCTACTCT 52488
TTGAATCGCTTACCTACTTGAGTCTTCAAGGAAACAAATTCAACGGGTCTATCCCTGCAA 52608
                                           tgaagtcacttgtttttttgcggcttaacgaaaaccgattgaccggtcctattcctagag 502
                                                                                                       CAGTTCTTGATCTTTCCAACAACAAATTCTCAGGTCAAATTCCTGCCTTGTTCTCCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-JAN 1998) to the DDBJ/EMBL/GenBank databases. Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of Gene Structure 2; 1532-3; Yana, Kisarazu, Chiba 292, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935, Fax:+81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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/clone_lib="Mitsui P1"
15130 c 15592 g 28056
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/strain="Columbia"
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Pred. No.
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                                                                  1445
                                                                                                                                       1385 TYCCCTTGGTGATTTGGAGCATCTTCTCAAGATGAACTTGAGTAGAAATCATATAACTGG
                                                                                                                                                                                                            1325 TATCGGTAACTTAGATACATTGGATCTTTCCAACAACAAGATAAATGGAATCATTCCTTC 1384
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Local Similarity 54.7%;
hes 146; Conservative
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12 1 (bases 1 to 3176)

13 Mitsukawa, N. and Robaato, E.U.

14 EXEMPTION OF PROTEIN CONTROLLING MORPHOGENESIS OF PLANT

15 PATENT: JP 197056382-A 1 04-MAR-1997;

16 CHIKYU KANKYO SANGYO GIJUTSU KENKYU KIKO, MITSUI GYOSAI SHOKUBUTSU

17 PATADIODPSIS thaliana (thale cress)

18 PN JP 1997056382-A/1

19 PN JP 1997056382-A/1

10 PP 14-AUG-1995 JP 1995216187

10 PP 14-AUG-1995 JP 1995216187

11 PP 14-AUG-1995 JP 1995216187

12 CC C12N15/09, A01H5/00, C12N5/10;

17 CC Strandedness: Double;

18 CC C12N15/09, Linear;

19 FH Key Location/Qualifiers

10 FFT Source (Organism='Arabidopsis thaliana' FT

11 Catalogical Coloradism (Arabidopsis thaliana' FT)
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               tgatttgtgtggaacaattccagtaga 575
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                                                             TGTAGTTCCAGGCGACTTTGGAAATCTAAGAAGCATCATGGAAATAGATCTTTCAAATAA 1504
                                                                                               tcctattcctagagaactcacagttatttcaagccttaaagttgttgatgtctcagggaa 548
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/strain='colombia'
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/db_xref="taxon:32644"
654 c 659 g 93
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Pred. No. 3.9e-07;
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/product='a
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D 20-NOV-1997.
D 20-NOV-1997.
F 13-MAY-1996; GB-010044.

R 14-MAY-1996; GB-010044.

PA (NOVS) NOVARTIS AG.

PI De Vries SC, Hecht VEG, Schmidt EDL, Van Holst GJ;

PR WF1; 98-086529/08.

PR P-PSDB; W47021.

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03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clone.
receptor kinase; apomixis; apomictic; seeds; production;
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
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03-Aug-1998 (first entry)
03-Aug-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous Es
receptor kinase; apomixis; apomictic; seeds
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Arabidopsis thaliana.
Cocation/Qualifiers
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2. 664
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20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
                                                                                            Production of apomictic seeds - useful in plant breeding Claim 28; Pages 79-80; 132pp; English.
The sequence is that of an EST clone showing high homolog SERK LRR (leucine-rich repeat) sequences.
Sequence 788 BP; 234 A; 191 C; 156 G; 207
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De Vries SC, Hecht VFG,
WPI; 98-086529/08.
P-PSDB; W47720.
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(NOVS) NOVARTIS AG.
De Vries SC, Hecht VF
WPI; 98-086529/08.
P-PSDB; W47022.
                                                                                                                                                                                                                                                                                                                           V06590 standard; cDNA to mRNA; 1063 BP. V06590; 03-AUG-1998 (first entry) Arabidopsis thaliana SERK LRR homologous receptor kinase; apomixis; apomictic; see plant breeding; leucine-rich repeat; ss. Arabidopsis thaliana.
production of apomictic seeds - useful in place Claim 28; Pages 86-88; 123pp; English. The sequence is that of an EST clone showing SERK LRR (leucine-rich repeat) sequences.
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E Arabidopsis thaliana SERK LRR homologous ES:
W receptor kinase; apomixis; apomictic; seeds;
Plant breeding; leucine-rich repeat; ss.
W Arabidopsis thaliana.
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20-W07-1997; E02443.
13-MAY-1996; GB-01044.
14-MAY-1996; GB-01044.
(NOVS) NOVARTIS AG.
(NOVS) NOVARTIS THE VFG, (PP-PSDB; W47019.
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The sequence is that of an EST clone showing high SERK LRR (leucine-rich repeat) sequences.
Sequence 981 BP; 286 A; 236 C; 180 G;
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Best Local S
Matches 532
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20-N0V-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-086529/08.
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Key Locat
CDS 142.
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The sequence is that of an EST clone showing high homology SERK LRR (leucine-rich repeat) sequences.
Sequence 1106 BP; 331 A; 258 C; 206 G; 311 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana SERK LRR homologous EST clone. receptor kinase; apomixis; apomictic; seeds; production; embryos; plant breeding; leucine-rich repeat; ss.
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03-AUG-1998
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acaacctgagattggagggaccagaactactaggtcttgcgagctatgacaccaattgca
                                                                          TGTGTGGGACAATCCCAACAAACGGACCCTTTGCTCACATTCCTTTACAGAACTTTGAGA
                                                                                                       tgtgtggaacaattccagtagaaggaccttttgaacacattcctatgcaaaacttttgaga
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71.9%;
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Pred. No. 9.2e-80;
0; Mismatches 115
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Ps Claim 27; Pages 91-95; 123pp; English.

Ct The sequence is that encoding SER, a putative receptor kinase.

Ct It may be used as part of a method of producing apomictic seeds

cc comprising: (a) transforming plant material with a nucleotide

sequence encoding a protein which in active form in a cell or

cell membrane renders the cell embryogenic; (b) regenerating

the transformed material into plants or carpel-containing

plant parts; and (c) expressing the sequence in the vicinity

of the embryo sac. The apomictic seeds and embryos thus produced

can be developed into plant progeny. This is useful in plant

breeding programs. Controllable and reproducible apomixis provides

cmany advantages in plant improvement and cultivar development in

the case that sexual plants are available as crosses with the

propagated hybrids and could shorten and simplify the breeding

process so that selfing and progeny testing to produce and/or

stabilise a desirable gene combination could be eliminated.

Apomixis allows plant breeders to develop cultivars with

specific stable traits for such characteristics as height,

seed and forage quality and maturity.

Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
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Best Local S
Matches 257
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Arabidopsis thaliana SERK greceptor kinase; apomixis;
plant breeding; ds.
Arabidopsis thaliana.
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20-N0V-1997; E02443.
13-MAY-1996; GB-010044.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
(NOVS) NOVARTIS AG.
DE VILES SC, HECht VFG,
WPI; 98-086529/08.
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cttgggaagcttgaacatttacaatatctgtatggaatcatcactcttttgccttttgat 258
                                                     catcaagtcactcgtctggatttggggaattcaaacttatctggacatctagtacctgaa 198
                                                                                                                                                                        GAAGGTGATGCTTTGCATACTTTGAGGGTTACTCTAGTTGATCCAAACAATGTCTTGCAG
                                     AACAGTGTCATAAGAGTTGATTTTGGGGAATGCAGAGTTATCTGGCCATTTAGTTCCAGAG
                                                                                                       AGCTGGGATCCTACGCTAGTGAATCCTTGCACATGGTTCCATGTCACTTGCAACAACGAG 398
                                                                                                                                                                                                                                          il Similarity
257; Conserv
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53.5%;
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                                                                                                                                                                                                                                        Score 106; DB Pred. No. 2.2e 0; Mismatches
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.2e-19;
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                                                                                                                                          Production of apomictic seeds - useful in plant breeding Claim 21; Pages 47-51; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant treading programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding seed process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;
                                                               Query Match
Best Local s
Matches 180
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20-NOV-1997.
13-MAY-1997; E
14-MAY-1996; G
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receptor kinase; apomixis; apomictic; seeds; production; embryos; plant breeding; ss.
Daucus carota.
Rey
Location/Qualifiers
CDS
94..1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG, Schmidt EDL, Van
WPI; 98-086529/08.
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                   gaactctacaaaaacgagattcaaaggaactataccttctgagcttggaaatctgaagagt 378
GAGCTTTACAGCAATAACATAAGTGGACCAATTCCTAGTGATCTTGGGAATCTGACAAAT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                               Similarity
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56.1%;
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                                                               Score 95.4; DB 1;
Pred. No. 1.5e-16;
0; Mismatches 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA emodding plant morphogenesis regulatory protein - useful to yield plants with short stems or altered inflorescence Claim 1; Pages 6-10; 17pp; Japanese.

The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to yield a plant with, e.g. short stems or altered inflorescence. The MRP catts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant.

Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;
                                                                                                                                                                                                                                                                                                                                     Query Match 8.3
Best Local Similarity 54.7
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J09056382-A.
04-MAR-1997.
24-AUG-1995; 216187.
24-AUG-1995; JF-216187.
(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
(CHK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
WPI: 97-206629/19.
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Arabidopsis thaliana plant morphogenesis regulatory protein cDNA.
Plant; morphogenesis; regulation; short; stem; alteration;
inflorescence; extraneous; gene; expression; transformation;
increase; control; form; length; ds.
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TTCCCTTGGTGATTTGGAGCATCTTCTCAAGATGAACTTGAGTAGAAATCATATAACTGG
                                                                                                            TATCGGTAACTTAGATACATTGGATCTTTCCAACAACAAGATAAATGGAATCATTCCTTC
                                                                                                                                          tctgaagagtctaatcagtttggatctgtacaacaacaatctcaccgggaaaatcccatc
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                                                                                                                                                                                                                                                                            gtcatatagtgaactctacaaaaacgagattcaaggaactataccttctgagcttggaaa
                                             ttotttgggaaaattgaagtcacttgtttttttgcggcttaacgaaaaccgattgaccgg
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/note= "plant morphogenesis regulatory protein"
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; Pred. No. 1.6e
0; Mismatches
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L.6e-10;
hes 121;
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     Production of apomictic seeds - useful in plant breeding
Sclaim 26; Pages 64-67; 123pp; English.
The sequence is that encoding SERK, a putative receptor kinase.
Claim 2be used as part of a method of producing apomictic seeds
Cc comprising: (a) transforming plant material with a nucleotide
cc cell membrane renders the cell embryogenic; (b) regenerating
Cc cell membrane renders the cell embryogenic; (b) regenerating
Cc the transformed material into plants or carpel-containing
Cc the transformed material into plants or carpel-containing
Cc plant parts; and (c) expressing the sequence in the vicinity
Cc of the embryo sac The apomictic seeds and embryos thus produced
Cc can be developed into plant progeny. This is useful in plant
Cc the case that sexual plants are available as crosses with the
cc apomictic plant. Apomixis provides for true-breeding, seed
Cc apomictic plant. Apomixis provides for true-breeding, seed
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V06585;
03-AUG-1998
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Key
CDS
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WPI; 98-086529/08.
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                                                                                                                                                                                           ) NOVARTIS AG.
les SC, Hecht VFG, Schmidt EDL, Van Holst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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GB-010044.
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ds.
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3731. .3802
/*tag= b
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/*tag= e
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/*tag= c
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/*tag= h_
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/*tag= f
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Sequence 4081 BP; 1120 A; 770 C; 785 G; 1406 T;
          T06307 is a tomato pathogen resisitance gene Cf-2.2 partial cDNA clone. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.2 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulvum. C.fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.
                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum.

W09531564-A2
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                                                                                                                                           p-pSDB; R85299.
Increasing plant pathogen resistance by induction of variegation may lead to acquired resistance to a broad range of pathogens.
Claim 9; Page 85-87; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            T06307
                                                                                                                                                                                                     (GATS-) GATSBY CHARITABLE Hammond-Kosack KE, Jones WPI; 96-010949/01.
                                                                                                                                                                                                                                                                                                                                                                             Partial tomato pathogen resistance gene Cf-2.2 cDNA clone. Pathogen resisitant; Cf-2.2; tomato; C.fulvum; Avr 4; Avr 9; fungal;
                                                                                                                                                                                                                                               31-MAR-1995; GB-006658.
07-APR-1995; GB-007232.
                                                                                                                                                                                                                                                                          11-MAY-1995; G01075.
11-MAY-1994; GB-009394
23-DEC-1994; WO-G02812
                                                                                                                                                                                                                                                                                                                                                                                                                                         T06307
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                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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   to attack 3573 BP;
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Pred.
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red. No. 5.2e
Mismatches
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Matches 136; Conserv
Query Match
Best Local Similarity
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11-MAY-1994; GB-009394.

23-DEC-1994; WO-G02812.

31-MAR-1995; GB-006558.

07-APR-1995; GB-007232.
                                               Increasing plant pathogen resistance by induction of variegation—may lead to acquired resistance to a broad range of pathogens.

Claim 9; Page 80-83; 131pp; English.

106306 is the tomato pathogen resistance gene Cf-2.1. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.1 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulum.

C. fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 6471 BP; 2073 A; 1106 C; 1122 G; 2170 T;
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Hammond-Kosack KE, Jones DA, WPI; 96-010949/01.
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Pathogen resisitant; Cf-2.1;
leaf mould; variegation; ds.
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1677. .1745
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1746. .5011
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1677. .5014
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5015. .
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7.48;
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e
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1; tomato;
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0; Mismatches
Score 66.4;
Pred. No. 1
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C.fulvum;
 DB 1;
.6e-08;
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           Length 6471;
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                                                                                     Disclosure; Fig 5, 75pp; English.

This sequence is a clone of the polynucleotide of the invention, which is able to confer pathogen resistance on a plant. The polynucleotide of the invention is one of two tomato CF-5 gene variants, which offer cresistance against the pathogen cladosporium fulvum-5. Transgenic plants can be produced by incorporating the gene into plant cells and cregenerating plants from the cells; asexually or sexually produced conferring can also be subsequently produced. Expression of the gene in confer pathogen resistance on a plant e.g. to tomato leaf complementary to the gene or fragments of it, are useful in anti-sense conferring pathogen resistance on plants acids/polynucleotides are useful as hybridisation probes to identify other genes/fragments of conferring pathogen resistance on plants e.g. Phytophthora resistance in contained to the sense of this class.

So Sequence 3541 BP; 1123 A; 630 C; 612 G; 1176 T;
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20-NOV-1997.
08-MAY-1997;
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V14522;
20-MAY-1998 (first entry)
CF-5 pathogen resistance gene clone Hcr2-5B gene.
Tomato; CF-5 pathogen resistance gene; Cladosporium tomato leaf mould; Bhytophthora resistance; ss.
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Key Location/Quali
CDS 603. .3002
                                                                                                                                                                                                                                                                                                                                                   Tomato gene Cf-5, confers resistance to Cladosporium fulvum - useful for production of transgenic plants resistant to pathogens e.g. tomato leaf mould C. fulvum in tomatoes Disclosure; Fig 5; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INNE-) INNES CENT INNOVATIONS LTD JOHN Dixon MS, Hatzixanthis K, Jones DA, Jone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-SEP-1996; GB-019924.
09-MAY-1996; GB-009681.
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 y Match 7.0%;
Local Similarity 52.5%;
hes 138; Conservative
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Score 63; DB 1;
Pred. No. le-07;
0; Mismatches 12
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(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-086529/08.
P-PSDB; W47013.
                                                                                                                                                                                                                                                                                                                                                                                                                             receptor kinase; a plant breeding; ds Daucus carota.
Key Lo
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13-MAY-1997;
14-MAY-1996;
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Production of apomictic seeds - useful in plant breeding Claim 21; Pages 40-46; 123pp; Engilsh.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Daucus carota
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        plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated.

Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
PT Tomato gene Cf-5, confers resistance to Cladosporium fulvum - useful production of transgenic plants resistant to pathogens e.g.

PT tomato leaf mould C. fulvum in tomatoes

PS Claim 3; Fig 1a; 75pp; English.

PS Claim 3; Fig 1a; 75pp; English.

CC This sequence is an example of the polynucleotide of the invention, and cis able to confer pathogen resistance on a plant. It is one of two tomato CC F-5 gene variants, which offer resistance against the pathogen CC cladosporium fulvum-5. Transgenic plants can be produced by incorporating CC the gene into plant cells and regenerating plants from the cells; CC asexually or sexually produced offspring can also be subsequently produced. Expression of the gene in plant cells can confer pathogen coligonucleotides with sequences complementary to the gene or fragments CC of it, are useful in anti-sense techniques to reduce gene expression. The cucleic acids/polynucleotides are useful as hybridisation probes to identify other genes/fragments conferring pathogen resistance on plants ce.g. Phytophthora resistance in potatoes. Homologies between Cf-5 and CC of any be used to identify further resistance genes of this class.

SQ Sequence 3979 BP; 1217 A; 717 C; 698 G; 1347 T;
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Tomato; CF-5 pathogen resistance gene; Cladosporium fulvum-5;
tomato leaf mould; Phytophthora resistance; ss.
Lycopersicon pimpinellifolium.
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V14518;
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20-NOV-1997.
08-MAY-1997; G01249.
24-SEP-1996; GB-019924.
09-MAY-1996; GB-009681.
(INNE-) INNES CENT INNOVATIONS LTD JOHN.
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transformed material into plants or carp
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20.NOV-1997.
08-MAY-1997; G01249.
24-SEP-1996; GB-019924.
09-MAY-1996; GB-019924.
09-MAY-1996; GB-10190; LTD J0
LIXON MS, HATZIXANTHIS K, JONES DA, J
WPI; 98-008895/01.
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Tomato; CF-5 pathogen resistance gene; Cladosporium fulvum-5; tomato leaf mould; Phytophthora resistance; ss.

Lycopersicon pimpinellifolium.
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CF-5 pathogen resistance q
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    ; Score 62.8; DB; Pred. No. 1.2e-0; Mismatches
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Pred. No. 1.2e-07;
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Search completed: June Job time: 40611 sec 23, 2000, 22:53:35



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Minimum DB
Maximum DB
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
6: /cgn2_6/ptodata/
7: /cgn2_6/ptodata/
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length: 1000000
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Match
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Listing first 45 summaries
        GenCore version
Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/lna/5C_COMB.seq:*
/cgn2_6/ptodata/2/lna/5C_COMB.seq:*
/cgn2_6/ptodata/2/lna/6_COMB.seq:*
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US-08-587-680A-3
US-08-475-891A-3
US-08-475-891A-1
US-08-587-680A-1
US-08-567-375-15
US-08-666-271-1
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US-08-938-534-27
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Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 27, Appli
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US-08-587-680A-24
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Patent No. 5182210	ມຸພ	Sequence 2, Appli	\mathbf{L}	Sequence 1, Appli	Sequence 1, Appli	Sequence 26, Appl	Sequence 47, Appl	Sequence 3, Appli	Sequence 44, Appl	Sequence 41, Appl	Sequence 38, Appl	Sequence 35, Appl	Sequence 1, Appli	Sequence 5, Appli	Sequence 5, Appli

ALIGNMENTS

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Sequence 24, Application US/08587680A
Patent NO. 5977448
GENERAL INFORMATION:
APPLICANT: Manig, Guo-Liang
APPLICANT: Ronald, Pamela C.
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Downsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: Son Francisco
STATE: California
COUVIRY: USA
ZIP: 94111-3804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION NUMBER: US 08/587,891
FILING DATE: 17-JAN-1996
CLASSIFICATION NUMBER: US 08/475,891
FILING DATE: 17-JAN-1995
PRIOR APPLICATION NUMBER: US 08/475,891
FILING DATE: 04-DEC-1995
PRIOR APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
PRIOR APPLICATION NUMBER: US 08/567,375
FRIING DATE: 04-DEC-1995
PRIOR APPLICATION NUMBER: US 08/567,375
FRIEDRONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
FULTER DAY (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
FULTER DAY (415) 576-0300
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TYPE: nucleic acid STRANDEDNESS: single

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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: 0
US-08-587-680A-24
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Best Local Similarity
Matches 131; Conserv
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                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ronald
APPLICANT: Wang,
                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
                                                                                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION UNMER: US 60/004,645
FILING DATE: 29-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Procedures and Materials for TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
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                NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34
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REFERENCE/DOCKET NUMBER:
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Pred. No. 4.3e-09;
0; Mismatches 115;
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Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLFOTTO
                               FILING DATE: 17-JAN-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1138 TTTCTTGCACTTGAATTGAATAAGATCACAGGAAGCATTCCGAAGGATATTGGCAATCTT 1197
                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1258
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LENGTH: 3921 base pair:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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APPLICATION NUMBER: US 08/373,375 FILING DATE: 17-JAN-1995
                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: join(1..2676, 3520..
OTHER INFORMATION: /product= '
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Song, Wen-Yuang
                                                                                                                                                                                                                                                 SSA
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                                                                                                                                                                                                                                                                                                   Townsend and Townsend and Crew LLP to Embarcadero Center, Eighth Floor
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                                                                         17-JAN-1996
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                                                                                         US/08/587,680A
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Pred. No. 1.1e-08;
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US-08-475-891A-3
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: LOCATION: join(1..2676, 3520..3918)
: OTHER INFORMATION: /product= "xa-21"
US-08-587-680A-3
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3921 bass -- Type:
                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Ronald,
APPLICANT: Wang, G
APPLICANT: Song, W
                                                                                                                                                                                                                           Sequence 3, Application US/08475891A Patent No. 5859339
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,375
PRIOR DATE: 04-DEC-1995
                                            NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in plants
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REGISTRATION NUMBER: 34,774
REFERENCE, DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1198 ATTGGCTTACAACATCTCTATCTCTGCAACAACAATTTCAGAGGGTCTCTTCCATCATCG 1257
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APPLICATION NUMBER:
                  493
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TYPE: nucleic acid
STRANDEDNESS: single
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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             San Francisco
California
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                                                                                                                                                                                           Ronald, Pamela C.
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Pred. No. 1
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L.1e-08;
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NAME: Bastlan, Kevin L.

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 0237C

TELECOMMONICATION INFORMATION:

TELECOMMONICATION TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                            Sequence 1, Application US/08475891A Patent No. 5859339
GENERAL INFORMATION:
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Best Local Similarity
Matches 135; Conserv
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Guo-Liang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
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NAME/KEY: CDS

LOCATION: join(512..3149, 3993..4393)

OTHER INFORMATION: /product= "RRK-B"

OTHER INFORMATION: /note= "xa21 xanthomonas spp. disease

OTHER INFORMATION: resistance gene RRK-B from rice (Oryza

OTHER INFORMATION: sativa)"
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/475,891
FILING DATE: 06-JUN-1995
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LENGTH: 5992 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          493
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 123;
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ADDRESSEE:

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. LOCATION: join(1648..4383, 5178..5513)
; OTHER INFORMATION: /product= "RRR-F";
; OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease;
; OTHER INFORMATION: resistance gene RRK-F from rice (Oryza;
; OTHER INFORMATION: sativa)"
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
              Sequence 1, Application US/08567375 Patent No. 5952485 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0237
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       2986
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MEDIUM TYPE: Floppy disk
APPLICANT:
                                                                                                                                                          3046 TTCAGTGGTTGGATACCA 3063
                                                                                                                                                                                                                                                                                                                  2926 TTGGGCAGGCTTAGAAACTTAGGCATTCTAGTCGCCTACGAAAACAACTTGAGCGGTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 tatagtgaactctacaaaaacgagattcaaggaactataccttctgagcttggaaatctg 372
                                                                                                                                                                                                                                                              493 attcctagagaactcacagttatttcaagccttaaagttgttgatgtctcagggaatgat 552
                                                                                                                                                                                                                                                                                                                                                        433
                                                                                                                                                                                                                                                                                                                                                                                                                      373 aagagtctaatcagtttggatctgtacaacaacaatctcaccgggaaaatccccatcttct 432
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 06-JUN
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nes 134; Conserv
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TOPOLOGY: linear
                                                                                                                                                                                           ttgtgtggaacaattcca 570
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California
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Ronald,
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Pamela C.
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Pred. No. 4.2e-08;
0; Mismatches 124;
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Best Local Similarity
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APPLICATION UNDEER: US 08/475,891
FRIOR APPLICATION DATA:
APPLICATION UNDEER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNDEER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Keytin L.
REGISTRATION UNDEER: 34,774
REFERENCE/DOCKET NUMBER: 023070-0588
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOM: (415) 576-0300
TELECAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
                                                                                                                                              2866
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CURRENT APPLICATION DATA:
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                                                               2926 TTGGGCAGGCTTAGAAACTTAGGCATTCTAGTCGCCTACGAAAACAACTTGAGCGGTTCG 2985
                                                                                                                                                                                                                                 2806 TTTCTTGCACTTGATTTGAATAAGATCACAGGAAGCATTCCAAAGGATATTGGCAATCTT 2865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                313 tatagtgaactctacaaaaacgagattcaaggaactataccttctgagcttggaaatctg 372
493 attectagagaaaeteacagttattteaageettaaagttgttgatgteteagggaatgat 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 6256 base pairs
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                                                                                                                                                                                                                                                                                                                  Conservative
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RMARION: /product= "RRK-F"

RWATION: /note= "Xa21 Xanthomonas spp. disease

RWATION: resistance gene RRK-F from rice

RWAȚION: (Oryza sativa)"
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Pred. No. 4.2e-08;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 29-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                   LOCATION: join(1648 OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                   LENGTH: 6256 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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T: Two Embarcadero Center, Eighth Floor
San Francisco
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Song, Wen-Yuang
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                                                                                                join(1648..4383, 5178..5513)
RMATION: /product= "RRK-F"
RMATION: /note= "xa21 xanthomonas spp. disease
RMATION: resistance gene RRK-F from rice (Oryza
RMATION: sativa)"
                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                         DNA (genomic)
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6.7%;
51.9%;
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Score 59.6; DB 4;
Pred. No. 4.2e-08;
                     Length 6256
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:

""""TOATION NUMBER: US 60/004,645
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                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/475,891

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA: US 08/373,375

APPLICATION NUMBER: US 08/373,375

FILING DATE: 17-JAN-1995

ATTORNEY/AGENT INFORMATION:
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                                                                                             TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                             TELEPHONE: (415) 576-0200
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CORRESPONDENCE ADDRESS:
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                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Procedures and Materials for TITLE OF INVENTION: Disease Resistance in Plants
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                                                                                                                                                                                TORNEY/AGENT TORNEY/AGENT L.
NAME: Bastian, Kevin L.
34,774
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 6
FILING DATE: 29-SEP-1995
                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
               STRANDEDNESS:
TOPOLOGY:
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                                                 831 base pairs
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Song, Wen-Yuang
                                                                                                               (415)
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               single
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                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,271
FILING DATE: 19-SEP-1996
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                                                               FILING DATE: 24-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9409363.0
FILING DATE: 11-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 23-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TELEPHONE: 703-816-4091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                              NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 62
                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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THOMAS, COLWYN M
JONES, DAVID A
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52.4%;
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No. 2.8e-08;
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Best Local Similarity
Matches 136; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/02812
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326428.1
FILING DATE: 24-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9409363.0
FILING DATE: 11-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
COMPUTER: FOR COMPATIBLE
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
CONFIGNATION UNITER. FOR 1666 27
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ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 NOI CITY: ARLINGTON
                                                                                                                                                                                                 APPLICATION NUMBER: US/08/666,271 FILING DATE: 19-SEP-1996
                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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THOMAS, COLWYN M
JONES, DAVID A
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                                                                                                                                       PCT/GB94/02812
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Pred. No. 1.5e
0; Mismatches
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1.5e-06;
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; NAME/KEY:
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US-08-666-271-1
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                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/0847353A Patent No. 5859338
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3905 base pairs
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                               APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2913 TATCAATCTCTCAAAGAACAGATTTGAAGGTCATATTCCAAGCATTATTGGAGATCTTGT 2972
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                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               555 gtgtggaacaattccagtagaaggaccttttga 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          495 tcctagagaactcacagttatttcaagccttaaagttgttgatgtctcagggaatgattt 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 gagtotaatoagittggatotgtacaacaacaatotoacogggaaaatocoatottottt 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3905 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                      CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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898..966
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967..3486
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898..3489
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PatentIn Release #1.0,
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Pred. No. 1.8e-06;
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Version #1.30
                                                                                                                                                              Albritton & Herbert
Suite 3400
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US-08-238-163-3
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                                                                                                                                                                                                                        Patent No. 5569830
GENERAL INFORMATION:
APPLICANT: BENNETT
APPLICANT: LABAVIT
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Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                                                                                                              Sequence 3,
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5733 base pairs
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APPLICATION NUMBER: US/00
ETILING DATE: 06-JUN-195
CLLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3120 CTACTACAACAGCTACACCGGTGGTGTTCCACGCGAGTTCGGTGGTTTAACAAAGCTTGA 3179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
                                                                                                                                  TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                     3360 AATCCC 3365
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3240 GAAACATCTACATACTCTGTTTCTTCACATCAACAACTTAACCGGTCATATACCACCGGA 3299
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COMPUTER READABLE FORM
                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                     564 aattcc
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LOCATION:
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REGISTRATION NUMBER: 38
REFERENCE/DOCKET NUMBER:
                                            ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 5733 base pairs TYPE: nucleic acid STRANDEDNESS: unknown
                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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              94105-1493
                                                                                                                                                                                                                                                                                                 Application US/08238163
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STOTZ, Henrik
                                                                                                                                                                                                                        BENNETT, Alan
LABAVITCH, John M.
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2434..5037
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5117..5467
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Pred. No. 5.5e-06;
0; Mismatches 121;
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PC-DOS/MS-DOS

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SOFTMARE: PALENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/ACENT. 800
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Best Local Similarity 48.
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    08-244-646-14
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                          TITLE OF INVENTION: Nucleotide Sequences Coding An TITLE OF INVENTION: Endopolygalacturonase Inhibitor NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                    COUNTRY: U:
ZIP: 80303
                                                                                          STATE:
                                                                                                                                          ADDRESSEE:
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                                                                                                                        E: Sally A. Sullivan
5370 Manhattan Circle Suite 201
                                                                      S
                                                                                                                                                                                                                                            Albersheim, Peter
Darvill, Alan
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421..1401
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Pred. No. 0.01;
0; Mismatches 119;
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APPLICANT:

APPLICANT

DONALD E. TRIMBUR GREGORY M. WHITED RICHARD D. LA REAU SHARON L. HAYNIE MARIA DIAZ-TORRES

VASANTHA

NAGARAJAN

APPLICANT:

APPLICANT:

APPLICANT:

CHARLES E. NAKAMURA ANTHONY A. GATENBY AMY (KUANG-HUA) HSU

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RESULT 14
US-088-563-5
US-08-968-563-5
; Sequence 5, Application
; Patent No. 6013494
; Patent No. IMPORMATION:
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LOCATION:
US-08-244-646-14
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Best Local Similarity 50.0
Conservative
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SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCI
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: SULLIVAN, Sally A.
REGISTRATION NUMBER: 32,06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,646
FILING DATE: 06-JUN-1994
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
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HYPOTHETICAL:
                                                                                                                                                                                                                                                      319 gaactctacaaaaacgagattcaaggaactataccttctgagcttggaaatctgaagagt 378
                                                                                                               439 aaattgaagtcacttgtttttttgcggcttaacgaaaaccggattgaccggtcctattcct 498
                                                                                                                                                                          895 CTGCAAAGTTTAAATGTGAGCTTCAACAATCTGTGCGGTGAGATTCCTCAAGGTGGGAAC 954
                                                                                                                                                                                              379 ctaatcagtttggatctgtacaacaacaatctcaccgggaaaatcccatcttctttggga 438
                                                                                                                                                                                                                                      835 GATCTGAGGAACAACCGTATCTATGGAACGCTACCTCAGGGACTAACGCAGCTAAAGTTT 894
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SOFTWARE: Patentl
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                                   Application US/08968563
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(303)499-8089
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Pred. No. 0.18;
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RESULT 15
5231168-1/c
;Patent No. 5231168
; Patent No. 5231168
; APPLICANY: DZIEGIEL, MORTEN;BORRE, MARTIN;JEPSEN, SOR
;VUUST, JENS;RIENECK, KLAUS;WIND, ANNETTE;JAKOBSEN, PALLE:
;TITLE OF INVENTION: MALARIA ANTIGEN
NUMBER OF SEQUENCES: 19
;CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/409,658
;FILING DATE: 18-SEP-1989
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; ORIGINAL SOURCE:
; ORGANISM: GPD
US-08-968-563-5
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/030,601
PILING DATE: NOVEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:

NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9982
REFERENCE/DOCKET NUMBER: CR-9982
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEPHONE: 302-892-8112
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1380 Dase pairs
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Best Local S
Matches 62
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STREET: 4 CAMBRIDGE PLACE
STREET: 1870 SOUTH WINTON ROAD
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: U.S.
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,563
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
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APPLICANT: STEPHEN K. PICATAGGIO
APPLICANT: RAMESCH V. NAIR
TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
TITLE OF INVENTION: PRODUCTION OF 1,3-PROPANEDIOL
                                                                                                                                                                                                                                                   539 GAGCTATCTCCTGTCTAAAGGGTTTTGAAGTTGGTGCTAAAGGTGT 584
                                                                                                                                                                                                                                                                               509 cagttatttcaagccttaaagttgttgatgtctcagggaatgattt 554
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Local Similarity 58.5%;
hes 62; Conservative
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Pred. No. 0.25;
0; Mismatches 44;
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Best Local Similarity
Matches 75; Conserv
2375 TITITITITITITIGITAATI 2355
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                                                                                                                   741 tgtttgtaaatctatatagagccttgtttcatgttatatatgaaagctttgagagacagt 800
                       861 tttgtgtttcttatgtaactt 881
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nilarity 53.2%;
Conservative
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Pred. No. 0.43;
0; Mismatches 66;
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Search completed: June 23, 2000, 22:46:00 Job time: 40306 sec



Run

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Post-processing: Minimum Match 0%
Listing first 45
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Perfect score:
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(without alignments)
584.592 Million cell updates/sec
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                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Query
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Minimum Maximum

Searched:

Sequence:

Database

REFERENCE 1 (bases 1 to 450) AUTHORS Newman, T., deBruijn.F.J., Green,P., Keegstra,K., Kende, I McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., The Retzel,E. and Somerville,C. TITLE Genes galore: a summary of methods for accessing results large-scale partial sequencing of anonymous Arabidopsis JOURNAL Plant Physiol. 106, 1241-1255 (1994)	ntae; matoph urosid	- '		41 147.8 16.5 368 64 AW032898 42 147.8 16.5 423 59 AI774881 43 147.8 16.5 423 62 AI896737 44 147.8 16.5 428 64 AW031917 45 147.8 16.5 497 59 AI772079	149.4 16.7 458 59 149.4 16.7 463 74 149.2 16.7 502 79 148.8 16.6 514 35	156.6 17.5 423 35 155.6 17.4 336 23 154 17.2 401 37 151.6 17.0 612 47	171.8 19.2 599 63 171 19.1 339 42 168.2 18.8 469 63 167 18.7 676 74	184 20.6 695 64 183.4 20.5 460 36 182.2 20.4 562 50 175.4 19.6 599 74 173.2 19.4 334 23	194.8 21.0 354 42 ALIUUB 194.8 21.8 579 43 AUG3129 189.4 21.2 417 21 D46231 189.6 20.9 616 42 AF07473 185.2 20.7 348 42 AII0068	204.2 22.8 545 64 202.6 22.7 305 25 199.2 22.3 511 74 197.6 22.1 714 64	209.6 23.4 570 50 208.6 23.3 541 64 207.8 23.2 637 80 205 22.9 646 74	6 220.6 24.7 608 7 219.6 24.6 720 8 213.8 23.9 430 9 210.4 23.5 657	419.8 47.0 450 20 387.4 43.3 443 63 265 29.6 556 23 256.4 28.7 353 23 273.8 75.0 534 33	DB I
omerville,S., Thomashow,M., accessing results from mous Arabidopsis cDNA clones	Streptophyta; Embryophyta; Tracheophyta; yta; Magnoliophyta; eudicotyledons; core is II; Brassicales; Brassicaceae;	06-NOV-1997 one SCH9T7P, mRNA		AW032898 EST276457 AL774881 EST255981 AL896737 EST266180 AW031917 EST275371 AI772079 EST2753179	AI777982 EST258861 AW221200 EST297669 AW286582 LG1_334_F C22372 C22372 Rice	C22371 C22371 Rice H37296 15425 Lambd AA712221 31949 Lam A1496325 sbb5c09.v	AW011134 S717B03 P AII00679 33B00 Lam AII92868 701493826 AW220075 ES7302558 AW72748 PS7755548	AW038168 EST279825 C72525 C72525 Rice AI691407 606015009 AW219797 EST302279 H37195 15324 Lambd	ALLUGES 33804 Lemi AUG31292 AUG31292 D46231 RICS19770A AF074734 AF074734 AI100682 33803 Lem	AW037836 EST279465 W65416 20456 Lambd AW221278 EST297747 AW030188 EST273443	A1676939 605047A07 AW036865 614019G10 AW350549 GM210009A AW221939 EST298750	AW443205 EST308135 AW031110 EST374417 AW307218 S554507.y AW350720 GM210009A	T04109 59 Lambda P A199615 70156713 R89998 16353 Lambd H37300 15429 Lambd AA344780 2542 Lambd	. 🖷
RESULT 2 AI999615/c AI999615 443 bp mRNA LOCUS AI999615 443 bp mRNA DEFINITION 701556713 A. thaliana, Columbia Col-0, rosette-3 Arabidopsis thaliana cDNA clone 701556713, mRNA sequence. ACCESSION AI999615	Qy 384 cagtttggatctgtacaacaacatctcacc-gggaaaatcccatcttcttt-gggaaaa 441		181 G	Qy 144 agtcactcgtctggatttggggaattcaaacttatctggacatctagtacctgaacttgg 203	Qy 84 ggatccaactcttgttaatccttgtacttggtttcatgtcacttgtaatcaacaccatca 143	Qy 24 ggacgctcttcacgcgcttcgccggagcttatcagatccagacaatgttgttcagagttg 83	Query Match 47.0%; Score 419.8; DB 20; Length 450; Best Local Similarity 98.4%; Pred. No. 3.6e-92; Matches 443; Conservative 0; Mismatches 5; Indels 2; Gaps 2;	Shlox-1 with (oligo dT primed) directional inserts cloned between the ECORI and HindIII sites. " BASE COUNT 125 a 94 c 81 g 147 t 3 others ORIGIN	grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The library was made in Novagen's Lambda	/clone_lib_"Lambda_FRL1" /note="Vector: Lambda Shlox-1; Site_1: EcoRI; Site_2: /note="Vector: Lambda Shlox-1; Site_1: EcoRI; Site_2: /indid FRL1 is a cDNA library derived from equal fundili; Lambda FRL1 is a cDNA. The mRNA sources were 1) 7 quantities of 4 pools of mRNA. The mRNA sources were 1) 7	/organism="Arabidopsis thaliana" /strain="var columbia" /db_xref="taxon:3702" /clone="SCH9T7P"	bm.cl.msu.edu. /Qualifiers	MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E. Lansing,Mi Tel: 517-353-0854	MEDLINE 95148729. COMMENT Contact: Thomas Newman

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388;
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On Mar 10, 1998 this sequence version replaced of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Mobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Warren, B., Ton, B., Krikorian, S., Elder, L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc. 4633 World Parkway Circle, St. Louis, MO 63134, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thale cress.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: psport; Site_1: NotI; Site_2: SalI; cDNA library was derived from untreated rosette tissue from Arabidopsis thallana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peat moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. cDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunted, ligated to SalI adaptors, digested with NotI, size-selected, and cloned into the NotI and SalI sites of the psport vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="A. thaliana, Columbia Col-0, rosette-3"
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/dev_stage="4 - 7 weeks"
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Pred. No. 2.8e-84;
0; Mismatches 42;
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313 tatagtgaactctacaaaaacgagattcaaaggaactataccttctgagcttggaaatctg 372
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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16353 Lambda-PRL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Thomas Newman MSU-DDE Plant Research Laboratory
MSU-DDE Plant Research Laboratory
Michigan State University
MSU-DDE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
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                                                                                                                        Similarity
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primer: T7 dye primer.
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larity 80.0%;
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/strain="var columbia"
/db_xref="taxon:3702"
/cione="187H5T7"
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/Clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox: Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox: Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox: Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox: Site_2: Si
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Pred. No. 1.6e
0; Mismatches
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Raikhel, N.,
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..6e-54;
nes 79;
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., Somerville,S., Thomashow,M.,
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95148729

On May 8, 1995 this sequence version replaced g1:801146.

Contact: Thomas Newman

MSU-DDE Plant Research Laboratory

MIChigan State University

MSU-DDE-PRL, Michigan State University, Plant Biology Bldg., E.
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primer: T7 dye primer.
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euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
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Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
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thes 261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTGGCAAAACCTGGAAATGGAGNAT
                                                                                                   D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Hansen,T.S., Ronning,C.M., Craven,M.B., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D., Giovannoni,J.J. and Martin,G.B. Generation of ESTs from tomato callus (mixed elicitor) Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:l135853.
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                            AW443205 608 bp mRNA EST EST308135 tomato mixed elicitor, BTI Lycopersicon clone_CLET43M10 5', mRNA sequence.
                                                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U.
                                                                                                                                                                                                                                                                                           Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core

eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Lambda-PRL2"
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0; Mismatches 65
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REFERENCE AUTHORS

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/db_xref="taxon:4081"
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/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF/"
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                                                                                               GAGCTCGGAAAGCTTGAACATCTACAGTATCTG------
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 agtgaactctacaaaaacgagattcaaggaactataccttctgagcttggaaatctgaag
                                                                                                                gaacttgggaagcttgaacatttacaattatctgtatggaatcatcactcttttgcctttt
                                                           gattatctgaaaacatttacattatcagtcacacatataacattttgctttgagtcatat
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AW031110
AW031110.1
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
On Dec 20, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation of ESTs from tomato callus tissue Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum
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                                                                                                                                                                                                                                                                                                                                                                Similarity
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864 656 4293
1: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; supplier: Giovannoni laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library" 149 c 143 g 228 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="tomato callus, TAMU"
/tlssue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF/"
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                                                                                                                                                                                                                                                                                                                                                 Score 219.6; DB 64;
Pred. No. 1.8e-43;
0; Mismatches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:113369(
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW307218 430 bp mRNA EST 20-JAN-2000 sf54c07.y1 Gm-c1009 Glycine max cDNA clone GENOME SYSTEMS CLOI Gm-c1009-3781 5' similar to TR:Q96477 Q96477 LRR PROTEIN. ;, i
                                                                                                                                                                                                                                                                                                                                         Email: estéwatson.wustl.edu
This clone is available through: Genome Systems, Inc.
This clone is available through: Genome Systems, Inc.
Parkway Circle St. Louis, Missouri 63134 For further i
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
seq primer: -40RP from Gibco
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Fax: 314 286 1810
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/lab_host="xti0-Goid"
/note="Yector: pBluescript II XR; Site_1: EcoRI; Site_2:
xhoI; The mRNA was isolated from entire roots of
2-month-old 'Williams' plants that were greenhouse grown
                                                                                                                     /clone="GENOME SYSTEMS
/clone_lib="Gm-c1009"
                                                                                                                                                                                      /organism="Glycine max"
/db_xref="taxon:3847"
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888) 919-3324 or (31)
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Pred. No. 4.5e-42;
D; Mismatches 97; Indels 0;
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Glycine max cDNA
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134. For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888)919-3324 or (314)
427-3324 or contact:clones@genomesystems.com or info@genome
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Seq primer: 5'-TTTTTTTTTTTTTTTTTT(A/C/G)-3'.
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131 c 120 g 191 t 25 others
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/db_xref="taxon:4577"
/db_xref="taxon:4577"
/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI; Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
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                                              ttgggaaaattgaagtcacttgtttttttgcggcttaacgaaaaccgattgaccggtcct 492
                                                                                                                                                                                                                                                                                                                                                                                     Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 9
Tel: 650 723 227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614019 row: G column: 10.
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On Jul 7, 1999 thi
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                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                   /tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
/note="forms"
                                                                                                                                                                                                                                        Lab
                                                                                                                                                                                                                                                   /note="Organ: root; Vector: pBlueScriptII SK+;
EcoRI; Site_2: XhoI; 3-4 days old root tissue:
                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
/cultivar="W23"
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/clone_lib="614 - roo"
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73.6%;
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phyta; Liliopsida; Poales;
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Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3136929.
Other ESTS: A1495378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae;
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Fax: (217) 333-4582
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/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; Library Gm-r1021 is a sequence-driven, reracked set of the original library Gm-c1004 which was prepared from root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Strategene's cDNA Synthesis xit (catalog #200401) was used to synthesize the cDNA. The Gm-c1004 library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Blology, Box5540, Northern Arizona University, Flagstaff, AZ 86011, email: paul.keim@nau.edu, virginia.coryell@nau.edu. The contig analysis to select unique genes was performed
                                                                                                                                                                                                                                                        /db_xref-"taxon:3847"
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/clone_lib-"Gm-r1021"
                                                                                                                                                                                                                     /tissue_type="root"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                              /organism="Glycine max"
/cultivar="Williams"
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313 tatagtgaactctacaaaaacgagattcaaggaactataccttctgagcttggaaatctg
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1 (hases I to 646)

1 (hases I to 646)

Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Bloth, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Bonning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
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Clemson University
100 Jordan Hall, C
                                                                                   On Jul 8, 1999 this s
Contact: David Frisch
                                                                                                                                       Generation of ESTs from tomato Unpublished (1999)
                                                      Clemson University Genomics Institute
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112 c 127 g 188 t 25 others
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/cultivar="TA496"
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313 tatagtgaactctacaaaaacgagattcaaggaactataccttcttgagcttggaaatctg
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Local Similarity 70.0 nes 275; Conservative
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Generation of ESTs from tomato leaf tissue monublished (1999)
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/fissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="%I1-Blue MRF'"
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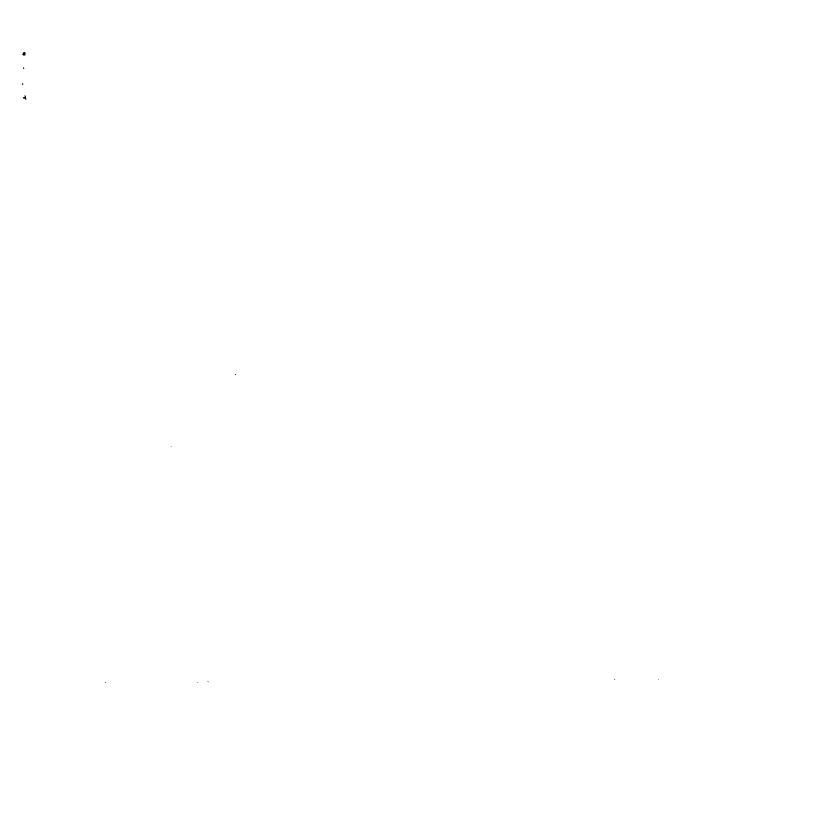
673 acttaaaaagaagttgaagaacctataaagaag

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428 TCTTAGAAGCTTGATGAATAGCTTCAGAAGAAG 460

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Arabidopsis thaliana
Residopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; eudicotyledons; core
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA (Plant Physiol. 106, 1241-1255 (1994)
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Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.
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20456 Lambda-PRL2
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primer: T7 dye primer.
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517-353-9168
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                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using olion of primed cDNA.
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50: gb_p13:*

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52: gb_htg8:*

53: gb_htg9:*

54: gb_htg10:*

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56: gb_htg12:*

57: gb_htg12:*

58: gb_htg13:*

58: gb_htg14:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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De, V.S., Schmidt, E.D., Van, H.G. al
PRODUCTION OF APOMICTIC SEED
PAtent: WO 9743427-A 20-NOV-1997;
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1 (bases 1 to 1106)

De, V.S., Schmidt, E.D., Van, H.G. a
PRODUCTION OF APOMICTIC SEED
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Query Match Best Local Similarity

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Score Pred.

912.4; DB 5; No. 1.3e-224;

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              aaatgaagaattggggggtgaccttgtaagaacacttcaccactttatcaaatatcacat
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    AATTACTCGGTCTTGCAAGCTACGACACTAACTGCACCTGAAACAACTGGCAAAACCTGA
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Local Similarity 96.1%;
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De, V.S., Schmidt, E.D., Van, H.G. a
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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/db_xref="taxon:32644"
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gctttgattcacctggtcgaagcaaactccgaaggagatgctctttacgctcttcgccgg
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Sequence 2
A67821
A67821.1
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De, V.S., Schmidt, E.D., Van, H.G. and PRODUCTION OF APOMICTIC SEED Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
                                                                                                                                                                                                                                                                                                       unidentified unidentified
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                                                      72.4%;
llarity 98.9%;
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                                                                                                                                      /note="unnamed protein product"
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LYKNNIQGTIPSELGNLKNLISLDLYNNNLTGIVPTSLGKLKSLVFLRLNDNRLTGPI
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/db_xref="taxon:32644"
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1 (bases 1 to 894)
De.V.S., Schmidt,E.D., Van,H.G. and
PRODUCTION OF APOMICTIC SEED
Patent: W0 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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Sequence 2
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphylicphytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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De,V.S., Schnidt,E.D., Van,H.G. a
PRODUCTION OF APOMICTIC SEED
Patent: WO 9743427-A 20-NOV-1997;
CIBA GEIGY AG (CH)
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RLANDDVMLLDWVKGLLKEKKLEMLVDPDLOTNYEBRELEOVIGVALLCTGGSPMER
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                   caagacaaccgcgtcactcgtgtggatttggggaattcaaacctctctggacatcttgcg
                                                                CTGCAGAGCTGGAATTCGACGCTTGCCAATCCCTGCACCTGGTTCCATGTCACCTGCAAC
                                                                                     AACACTGAAGGTGACATACTGTACAAGCAAAGGTTGGCATGGGAGGACCCAAACAACGTG
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1997 Mar;10(2):302]]
2  (bases 1 to 936)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hipskind, J.D., Nicholson, R.L. and Goldsbrough, P.B. Isolation of a cDNA encoding a novel leucine-rich Sorghum bicolor inoculated with fungi Mol. Plant Microbe Interact. 9 (9), 819-825 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-JUN-1996) John D. Hipskind, Botany and Plant Pathology, Purdue University, West Lafayette, IN 47907, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
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                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAC49559.1"
/db_xref="GI:1710124"
/db_xref="GI:1710124"
/translation="MAPCPFAAAGFLTGLLALATFASCNTEGDILYKQRLAWEDPNNVL
/SWNSTLANPCTWFHYTCNNNNFVIKYDLGNAGISGFLLPDLAEIQNLQYIELYGNGL
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LTSLLESKLQENSLSGAIPASLGNIKALQFSRLNDNMLTGTVPSKSFFLSTFGNLTEL
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232 c 207 g 250
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/note="leucine-rich repeat-containing extracellular
/logrotein; contains six N-glycosylation sites
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/db_xref="taxon:4558"
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1 (bases 1 to 1755)

Schmidt E.D., Guzzo, F., Toonen, M.A. and de Vries, S.C.

A leucine-rich repeat containing receptor-like kinase marks somatic plant cells competent to form embryos
Development 124 (10), 2049-2062 (1997)

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Schmidt, E.D.L., Guzz
Direct Submission
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Submitted (12-MAR-1997) Molecular Biology, Ac
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RFSLKELQVARTDFST1LGRGGFGKVVKGRLAAGSLVAAVKRLKERTPGGELQFQTEV
EMISMAVHRULLRLAGFCMFPTERLLJYPYMANGSVASCLRERQPSEPPLDWPTRKI
ALGSARGLSYLHDHCDPKIIHRDVKAANILLDEEFEAVVGDFGLARLMDYKDTHVTTA
                                                                                                                                                                  /translation-"MNRNSINILNYMQFTDAYLDKYGVLMTLELYSNNISGPIPSDLG
NLTNLVSLDLYMNSFSGPIPDTLGKLTRLRFLRLNNNSLSGPIPMSLTNITTLQVLDL
SNNRLSGPVPDNGSFSLFTPISFANNLNLCGPVTGRPCPGSPPPSPPPPFIPPSTVQP
                                                                                                                                                                                                                       /product="somatic embryogenesis receptor-like
/protein_id="AAB61708.1"
/db_xref="GI:2224911"
                                     LAEKWDEWQKVEVIHQDVELAPHRTSEWILDSTDNLHAFELSGPR"
                                                      VRGTLGY IAPEYLSTGKSSEKTDVFGYG IMLLEL ITGQRAFDLARLANDDDVMLLDWV
KSLLKEKKLEMLVDPDLENNY IDTEVEQL IQVALLCTQGSPMERPKMSEVVRMLEGDG
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/db_xref="taxon:4039"
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Query Match
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Score 103.4; DB 8; Pred. No. 2.4e-16; 0; Mismatches 161;

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Eukaryota; Viiidiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
1 (bases 1 to 1815)
De,V.S., Schmidt,E.D., Van,H.G. and Hecht,V.F.
PRODUCTION OF APOMICTIC SEED
Patent: W0 9743427-A 20-NOV-1997;
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PGQNGPTGAIAGGVAAGAALLFAAPAMAFAWMRRKFPREHFTDVPAEEDDFUHLGQLK
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KSILKEKKLEMLVDPDLENNYIDTEVEQLIQVALLCTGGSPMERPKMSEVVRMLEGDG
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94. .1755
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                                                                                                                                                                                                                                                                                                        /note="unnamed protein product"
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                                                                                                                                                                                                                                                                                      Submitted (18-JAN-1996) P. Vera, Universidad Politecnica de Valencia, Inst. de Biologia Molecular y Celular de Plantas, C de Vera 14, E- 46022 Valencia, SPAIN

2 (bases 1 to 4604)

Tornero, P., Mayda, E., Gomez, M.D., Canas, L., Conejero, V. and V Characterization of LRP, a leucine-rich repeat (LRR) protein tomato plants that is processed during pathogenesis
Plant J. 10 (2), 315-330 (1996)
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X95269.1 GI:1619299
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                                                                       113. .4355

/gene="LRP"

join(113. .34

4283. .4355)

/gene="LRP"
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Arabidopsis.

1 (bases 1 to 101284)

Lin.X., Kaul.S., Town,C.D., Benito,M., Creasy,T.H.,
Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Be
Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                ATAC009991 101284 bp DNA PLN 08-OCT-1999 ATACHOPSIS thaliana chromosome III BAC F9F8 genomic sequence,
                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Arabidopsis thaliana
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AC009991.3 GI:6016677
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ELYKNNIQGTIPKELGNLKSLISLDLYNNNISGTIPTSLGNLKNLVFLRLNDNKLTGP
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/gene="LRP"
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/gene="LRP"
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/gene="LRP"
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/gene="LRP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TICR (http://www.tigr.org/rdb/ak/at.html).

Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding trans are predicted by transacan-SE (Sean Eddy, http://genome.wustl.edu/eddy/transcan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions of http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov). Genefinder (Phila Green, University of Washington), Genscan (Chris Burge, Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROCKWILE, MD 20850, USA
e-mail: xiin@tigr.org
BAC clone F9F8 is from Arabidopsis chromosome III and is near the
molecular marker g4547.
The orientation of the sequence is from SP6 to T7 end of the BAC
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Direct Submission
Submitted (09-SEP-1999) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org
3 (bases 1 to 101284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic sequence that are not annotated as genes but
exons by GRAIL are annotated as misc features.
   Location/Qualifiers
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-OCT-1999) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA On Oct 8, 1999 this sequence version replaced gi:5902413. Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana chromosome III BAC F9F8 genomic sequence Unpublished
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                                                                                                                    854. 973
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/note="exon predicted by xgrail, marginal_shadowexon"
                              complement(1516...1694)
/note="exon predicted by
excellent_shadowexon"
1546...1666
                                                                                                                                                                                                                                                                /note="ex
672. .752
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excellent_shadowexon"
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                                                                                                                                                                                                                                                                                                                                                                                                                        /note="exon predicted by xgrail, quality excellent"
124. .259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis
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                                                                                                                                                                                                                                   note-"exon predicted by xgrail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="F9F8"
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                                                                                                                              complement(<9426. .>11865)
/gene="F9F8.3"
/note="similar to leucoanthocyanidin dioxygenase
GB:BAA20143 [Perilla frutescens]"
complement(join(9426. .9674,10198. .10528,11098.
11491. .11865))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to nucleic acid binding protein Alfin-1 GB:AAA20093 [Medicago sativa]" join(5696. .5795,5897. .5929,6013. .6235,7264. .7387,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MVGPARPQIVLFGSSIVQMSFGHGGWGAILSEVYARKADIILRG
YYGWNSSRALEVUDQVFPKDAAVQPSLVIVYFGGNDSMAPHSSGLGPHVPLTEYVDNM
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QELGLEVVDLFSTFQKADDWKTVCFTDGIHLSAQGSKIVAGEILRVVKEAEWHPSLHW
KSMPTEFADDSFYDLVSADGKQTVNSSEWTIFWEEQWD"
complement(5513..5597)
/ipt_family="(GA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (5527. .5579)
/note executed by xgrail, quality
excellent_shadowexon
join (5589. .5795,5897. .5929,6013. .6235.
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complement(2090. .2250)
/product="putative leucoanthocyanidin dioxygenase"
/protein_id="AAF01507.1"
/protein_id="AAF01507.1"
/db_xref="Gui:6016680"
/translation="MNNLDEIKIESKTCLNDQEQEVKIDNMHMSDQDKNKIEIKNKSG
/translation="MNNLDEIKIESKTCLNDQEQEVKIDNMHMSDQDKNKIEIKNKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCVKITPAKAESIKQYKCPPCCAKKGRQ" complement(7717. .7760)
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LLSVSFYFGARLNRNERKRLFSLINDLPTLFDVVTGRKAMKDNKPSSDSGSKSRNGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative nucleic acid binding protein"
/protein_id="AAF01506.1"
/db_xref="GI:6016679"
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                                                                                                                                                                                                                                                                                 /gene="F9F8.3"
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/db_xref="GI:6016678"
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/note="unknown protein"
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4506. .4655,4800. .5013)
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2114. .2246
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                                                                                                                                                                                                                                                                                                                                                                                      lement(7810. .7847)
_family="(GAAAA)n"
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lement(join(<9426. .9674,10198. .10528,11098. .11345,
1. .>11865))
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3070. 2007
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.4655,4800. .>5013)
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44816 TCTTACAGGTTGATTCCAATAAGCTCAGTGGAAATGTTCCCCATCTCACTACTGAATTTGA 44757
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                                                                                                                                                                                                                                                                                                                                                                     44876 CTTACAACAATTTCGTTGGTGAAATCCCATCTTCTTTTGGCAATCTAAACCAGCTGATCG
44696 TCAGTTTACTATCAAACTTGATGGACTTTGAAGCAAGTAACAACGCTTTCACTGGAACTC 44637
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                                                                                                                                                                                                                                                                                                                                                                                                                         410 acasasacacaca; ccaaggaactataccttccgaacttggaaatctgaagaatctcatca 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y Match 8.0%;
Local Similarity 54.9%;
                                          tcactgcaatcccaagccttaaagttgttgatgtctcaagcaatgatttgtgtggaacaa 649
                                                                                                                                                            agtctctggtcttttttacggcttaatgacaaccgattgacggggccaatccctagagcac 589
                                                                                                                                                                                                                                                                                    CGAGGTTGTCTGCTTTATTACTTTCCCACAATCAGTTCACAGGCACGATTCCTAATAACA 44697
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/note="exon predicted by xgrail, quality marginal"
complement(13742. .13788)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Protein_1d-"AAF01508:1"
/Protein_1d-"AAF01508:1"
/db_xref-"G1:6016681"
/translation-"MAMIVILSEGIRDLPRIYTTPRSNFLSNNNKFRPSLSSSYKTS
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AAIPKHCWVKNPWKSLSYVVRDVAIVBALAACAAYLNNWIVWFLYWLAQGTMTWALFV
LGHDCGHGSFSNDPKLNSVYGHLLHSSILVPYHGWRISHRTHHQNHGHVENDESWHPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="exon predicted by xgrail, quality marginal" complement(join(13822. .14179,14261. .14398,14502. .14582, 14676. .14861,14941. .15033,15124. .15190,15272. .15361,
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/note="exon predicted by xgrail, quality marginal_shadowexon"
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/rpt_family="(GA)n"
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GGMTILLPDDQVVGLQVRHGDTWITVNPLRHAFIVNIGDQIQILSNSKYKSVEHRVIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(13988. .14179,14261. .14398,14502. .14582, 14676. .14861,14941. .15033,15124. .15190,15272. .15361, 15662. .16155))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="identical to omega-3 fatty acid desaturase, chloroplast precursor GB:P46310 [Chloroplast Arabidopsis thaliana]"
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PRTYEGYGSRLGVEKGAILDWNDYYYLHFLPLALKDFNKWPSLPSNIREMNDEYGKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEKIYNTLDKPTRFFRFTLPLVMLAYPFYLWARSPGKKGSHYHPDSDLFLPKERKDVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="omega-3 fatty acid desaturase,
precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(13822. .16380)
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/gene="F9F8.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 84.8; DB 8;
Pred. No. 1.7e-11;
0; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 101284;
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AC008017.2
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euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (18-SEP-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Brooks, S., Buehler, E., Chao, Q., Dunn, P., Gonzalez, A., Khan, S., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shin, P., Toriun, M., Vyotskala, V., Yu, G., Ecker, J., Theologis, A. and Tayla B. w., Vyotskala, V., Yu, G., Ecker, J., Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-JUL-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-JUL-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15,
                                                                                                                                                                                                                    /note="81% identical to threonine synthase [Arabidopsis thaliana] (gi|4914408). Location of ests GBGF589 3' (gb|F15267) and GBGe175 (gb|Z26034)" /codon_start=1
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/product-"Putative threonine synthase"
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/protein_id-"AAD55628.1"
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/translation-"MASFSLPHSATYEPSHSETSLKPHSAASETVRCTSASPAVPPQT
/translation-"MASFSLPHSATYEPSHSETSLKPHSAASETVRCTSASPAVPPQT
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DQRPRASPDENIRDEARRRPHOLQNISARAYVPFNAPPSSTESYSLDEIVTRSQSGALL
DQRHDFAALKRYDGEFWRLFDSRVGKTUMPVSGGVMSKEWYLPEIDDDIVSAFEA
NSNLFWAERFGKQYLQMNDLMVKHCGISHTGSFKDLGMSVLVSQVNRLRKMNKPVIGV
                                                                                                                                                                                                                                                                                                                                                                                                              complement(1333. .2966)
/gene="F3N23.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone-"F3N23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999 this sequence version ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gi:5441915
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      gene
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/transiatation-"MASSSSSATRLRHYDVFLSFRGVDTRQTIVSHLYVALRNNGVL
TFKDDRKLEIGDTIADGLVKAJOTSWFAVVILGENYAJSTRCLEELRLIKQLHSERQI
KVLPIFYGVKFSDVRYQEGSFATAFQSVDEADMIAEVVGGISSRLPRMKSTDLILLVG
MEAHMXKMTLLLNIGCEDEVHMIGIWGMGGIGKSTIAKCLYDRFSRGFPAHCFLENVS
KGYDIKHLQKELLSHLLYDEDYELMSWEAGSQEIKERLGHGKVFVVLDNVDKVEQLHG
LAKDPSWFGPGSRIIITTRDKGLLNSCUNIVEVKCLDDKDALQVFKKLAFGGRPPS
DGFEQLFIRASRLAHGLPSALVAFASHLSAIVAIDEWEDELLALETFOQKNVQEILRA
SYDGLDQYDKTVFLHVACFFNGGHLRYIRAFLKNCDARINHLAAKCLVNISIDGCISM
HILLVQTGREIVRQESDWRPSKORFLKMPTEIHTVYLDSWFHLGGRVSNLQLISDDYVL
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NLRELPELSTAVNLEELILESCTSLVQIPESINRLYLKKLMMMYCDGLEGVILVNDLQ
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DICQLOLLETLDGGNDFVYLPFSMGQLAMLKYLSLSNCRRLKALPQLSQVERLVLSG
CVKLGSLMGILGAGRYNLLDFCVEKCKSIGSLMGILSVERSAPGRNELLELSLELENGKS
CVKLGSLMGILGAGRYNLLDFCVEKCKSIGSLMGILSVERSAPGRNELLELSLELENGKS
CVKLGSLMGILGAGRYNLLDFCVEKCKSIGSLMGILSVERSAPGRNELLELSLELENGKS
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complement(join(8272. .8658,8746. .8916,
9161. .9252,9364. .9661))
/gene="F3N23.3"
/note="99% identical to Transcription fa
thallana) (gi12398525)."
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6030. 7079
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LVNASRCNYVNGFDAFRKIVRADGPKGLYRGFGISIMLAFSNAVWHASYSVAQRMVW
GGIGCYVCKKDEESGNNSTTMKPDSKTIMAVQGVSAALAGSVSALITMPLDTIKTRLQ
VLDGEDSSNNGKRGPSIGQTVRNLVREGGWTACYRGLGPRCASMSMSATTMITTYEFL
KRLSAKNHDGFYSKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(12076. .16057)
/gene="F3N23.4"
complement(join(12076. .12519,12613. .13851,13955. .14140,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mmHQMLNKKDSATHSTLPYLNTSISWGVVPTDSVANRRGSAESL
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RHVHALKRPRGSGGRFLNTKKLLQESEQAAAREQEQDKLGQQVNRKTNMSRFEAHMLQ
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HLIREVTAELDIYLANSLNSLELEGQKTAALIEILQOFWQVPDWVIVPGGNLIGNIYAF
YKGFENCKELGVDRIPALVCAQAMANPLYLHYKSGFKEDENFLKANTTFASA1QI
DPVSIDRAVYALKKSNGIVEEATEEELMDATALADSTGMFICPHTGVALTALMKLRKS
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/protein_id="AAD55630.1"
/db_xref="GI:5903072"
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                                                                                                               KYLYAHGCESLEHVNFSSNHSFNHLDFSHCISLECISDLVRDFMNBEYSQEAPFRLVC
ITKYSIASTNNMRTSWREPMRIKLPKIKAAPKLVGFFVQIMVVCEKPFHLQFPAFSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Similar to disease resistance proteins"
/protein_id="AAD55631.1"
/db_xref="GI:5903073"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Similar to disease resistance proteins RPP1-WsB (gi13860165), RPP1-WsC (gi13860167) and RPP1-WsA (gi13860163) [Krabidopsis thallana]."
/codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNKDRSSTTSGSDITSVSDGADIFGHTEFQFSGFPTPINRAMLVHGQSNDMHGGGDMH
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/db_xref="GI:5903071"
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(gb|H77203) and 205D12XP 3' (gb|AA605559)"
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HIQVPEPGDEIILCGVEHVGFVLK"
16543. .17907
                                                                                                                                                                                                    LVSLSEELSHFTKLTYLDLSSLEFRRIPTSIRELSFMRTLYLNNCNKIFSLTDLPESI
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hes 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCTGAAGCCACTCCATGTAACTGGTTTGGTATTATCTGTGATGATTCTAAGAAGGTTA 84582
                                                                      GTTTAGGGAACTGTAGCTCACTTGTGTACATTGATTTGTCTGAAAATAGTTTCTCTGGTA 84762
                                                                                                                                            aacttggaaatctgaagaatctcatcagcttggatctgtacaacaacaatcttacaggga 502
                                                                                                                                                                                                                       TCABAAGCTTAGAGATATTGGATATGAGTTCTAACAATTTCTCTGGGATTATACCTTCCA 84702
                                                                                                                                                                                                                                                                                                                                                                    CGTCTCTCAACTTCACCGGTTCAGGTGTTTCAGGCCAATTGGGTCCTGAAATAGGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                           tagttcccacttctttgggaaaattgaagtctctggtctttttacggcttaatgacaacc 562
                                                                                                                                                                                                                                                                  ttgaacatttacagtatctagagctctacaaaaacaacatccaaggaactataccttccg 442
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/gene="F3N23.6"

/gene="F3N23.6"

/gene="F3N23.6"

/gene="F3N23.6"

/gene="F3N23.6"

/gene="F3N23.6"

/gene="F3N23.6"

/note="Similar to entire sequence of downy mildew
/note="Similar to RPP5 [Arabidopsis thaliana]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVRTVYEVKCHUNDAALQLFNQLAFKGALPPSELYEKLSIRASWLAGGLPVALEAYGL
FORRWISLKEMPDALCEFIEAPDESYMEILKISYDGLEETDKWYELBYGACLFNGEPLR
RATTLLDDGVLQGCLGKILAEKSLIEITASGYIKHMILVDQTARAIVNGESMORRHG
RGVLWAPPYEIVELKRHYEILAEKSLIEITASGYIKHMILVDQTARAIVNGESMORRHG
ILAIFLFYEYLAGGMPNLRRLDLSDSENLEQLPDLSMAVNLEELITQGCKRLKKIPES
ISYLTRLITLDVSYCEELASYITIRELMRSGROIALYFSGKEVETRSIANLSIGGNIH
IQMFWLDGNVDHLSFTTEQQGPDKLTKKEKQAAFGELKKEQQQEPKKTILCGFGSL
MRKGRKVKATSEFLDHEWMMQRDOLAPDNQAALEFSTTRQAALOFLPETHGOESVKKA
QGKSQPTSKFHGFTSVDISRFRYSSDGASFLCFSLSMFPCVKELILINLNIKVIPDDV
GGIKFLEKLDWSGNDFETLPETMNQLFRLKYASFRNCCRLKALPALVQLETIKLSGGI
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ddkkleigdsiseeisraiqustyalvilsenyasskcldelakwymdlhkknikkvy
pirygddshrhqtgsftdkyqdskmpnkyttwrealtigllakagkdfetceber
pirygddshrhqtgsftdkypdskmpnkyttwrealtiglakagkdfetceber
MIEEIVKDISKKLLMQDVDF5DIVGNNAHMERLSPLLSMDSEMEVRNIGIWGMGIA
KTTIAKCLFDQFSQGFpARCFLENVSKIYRKGGVSSLAEKFLSTTLGLSKKKMKGSGV
KTTIAKCLFDQFSQGFPARCFLENVSKIYRKGVSSSMFGFGSIIITTRALKTLANKGLNTY
KLGPQBIKARFGCRKVFVVLDNVDDMAQMHAFAQESSWFGFGSIIITTRACKILLTY
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//db_xref="G1:5903074"
//db_xref="G1:5903074"
//db_xref="G1:5903074"
//db_xref="G1:5903074"
//db_xref="G1:5903074"
//db_xref="G1:5903074"
//db_xref="G1:590X070"
//db_xref="G1:590X07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Similar to part of downy mildew resistance protein RPP5"
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join(16543. .16961,17058. .17907)
/gene="F3N23.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCFGLKRDEHLIAQFLNEGENEEESLGFAFFPGTEVPSYFDHIDKGKSLTIDLPQIWP
SPKLLGFDACVVIACERPFDIQFSPFSYDWDWGYERYFCLYLKPDFHSTDPSTEDEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (gi|2109275)."
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81.6; DB 8;
Pred. No. 1.1e-10;
0; Mismatches 214;
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84763 AGGTCCCCGATACTCTCGGTAGCTTGAAGAGCTTGGCCGATTTGTATCTTTACAGCAACT 84822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-NOV-1996) USDA, ARS, Appalachian Fruit Research Station, 45 Wiltshire Road, Kearneysville, WV 25430, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 5033)
Bassett,C.L., Cohen,R.A., Nickerson,M.L. and Rajeevan,M.S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bassett,C.L., Cohen,R.A., Nickerson,M.L. and Rajeevan,M.S. Identification and Preliminary Characterization of an Unusual Leucine-rich Repeat Receptor-like Protein Kinase from Morning Glory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Convolvulaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                  nil receptor-like protein kinase (inrpk1) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:35883"
/tissue_type="young leaf"
237 .251
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SILRPCNMQSNTGKGGLSTLGIAMIYLGALLFIICLFLFSAFLFLHCKKSVQEIAISA
QEGDGSLLNKVLEATENLNDKYVIGKGAHGTIYKATLSPDKVYAVKKLVFTGIKNGSV
                                                                                                                                                                                                                                                                                                               /product="receptor-like protein kinase"
/protein_id="AAB3558.1"
/db_xref="G1:1684913"
/translation="MKVAVNTFLLSLCSTSSIYAAFALNSDGAALLSLTRHWTPIPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1144. .4566
/gene="inrpk1"
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/cultivar="Violet"
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/gene="inrpk1"
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                                                                                                                                  1 (bases 1 to 81513)
Liu,S.X., Sakano,H., Yu,G., Lee,J.M., Lenz,C., Pham,P., Toriumi, Chin,C., Chiou,J., Chii,E., Chung,M., Gonzalez,A., Howng,B., Liu,A., Vaysberg,M., Altafi,H., Brooks,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N.F., Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Miranda,M., Nguyen,M., Pala,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R., Federspiel,N.A. and Theologis,A.
Submitted (15-JAN-2000) Plant
Street, Albany, CA 94710, USA
3 (bases 1 to 81513)
                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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TRHNIAVGTAHGLAYLHFDCDPA VYHRIK PMYILLDSDLEPH ISDFGTAKLLDQSAT
SIPSNTVQGTIGYMAPENATTTVKSRESDVYSYGVYLLELITKKKALDPSFNGETDIV
GWVRSVMTQTGEIQKIVDPSLLDELIDSSVMEQVTEALSLALRCAEKEVDKRPTMRDV
VKQLTRWSIRSYSSSYRNKSK"
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Li Submitted (09-FEB-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
On Feb 11, 2000 this sequence version replaced gi:6693723.
The sequence is of BAC F1407 from Arabidopsis thaliana chromosome
1. The sequence does not represent the sequence of the entire
insert of this clone. It is shorter by 6954 bp because we submit conly the unique sequence of the clone. However, in order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide small overlaps (200 bp) between overlapping sumbitted clones. The 5' end of this sequence overlaps by 200 bp to the 3' end of the sequence of the clone
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Arabidopsis thaliana ch
complete sequence.
ACO11765.4 GI:6539234
Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B., Ronning,C.M., Koo,H., Fujli,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome I BAC FIM20 genomic sequence Unpublished
                                                                                                                                                      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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/cultivar="Columbia"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes were identified by a combination of three methods: Gene prediction programs including GRAII (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/~chris/CENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions of expons to Genes that are not annotated as genes but have predicted expons by GRAII.are annotated as misc, features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rockville, MD 20850, USA
e-mail: xiln@tigr.org
BAC clone FIM20 is from Arabidopsis chromosome I and is near the
molecular marker mi425.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-DEC-1999) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA On Dec 8, 1999 this sequence version replaced gi:6102640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission Submitted (14-CCT-1999) The Institute for Genomic Research, Submitted enter Dr. Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 134402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Dec 8, 1999 this sequence vo
Address all correspondence to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLone
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Medical Center Dr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'clone="F1M20"
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VRLPALQREEAWFLGTVRIGKKWLGHGLKKVKESEIKGLADSNSTLSQISCHRKAGNE
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VRLPALGESTIPSAEDIEQEIQHEKLDSPARDRDEHLTYGLSNSGLCLLSLARLVSESRPC
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GCETLTORG
                                                                                                      8771. .8827 recurred by xgrail, /note="exon predicted by xgrail, marginal_shadowexon" 8935. .9008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(4069 .4131)
/note="exon predicted by xgrail, quality excellent"
complement(join(<4608. .4760,4885. .>4974))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5111. .5190)
/note="exon predicted by
complement(<5342. .>7603)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(4608. .4760,4885. .4974))
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SVKFMÅRETLILRRLNHPNITKLEGLITSKLSCNIQLVFEYMEHDLTGLLSSPDIKFT
TPQIKCYMKQLLSGLDHCHSRGVMHRDIKGSNLLLSNEGILKVADFGLANFSNSSGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative protein kinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(1655. .17
2679. .2963,3052. .3429))
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protein kinase domain"
9333. . 9000 M333 . . 9000 your predicted by xgrail, quality marginal_shadowexon"
9421. .9528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<5342. .>7603)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative dolichyl-phosphate mannosyltransferase
polypeptide 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to dolichyl-phosphate mannosyltransferase
polypeptide 2 GB:4503365 [Homo sapiens] (regulator of
dolichol phosphate-mannose synthesis: EMBO J 1998 Sep
1;17(17):4920-9)"
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HKRCTASSALVSQYFTTKPFACDPSSLPIYPPSKEIDTKHRDEAARSVISFIT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKPLTSRVVTLWYRPPELLLGATDYGASVDLWSVGCVFAELLLGKPILRGRTEVEQLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by xgrail, quality excellent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1777,1908. .2135,2258. .2581,
                                                                                                                                                                 quality
                                                                                                                                                                                                                                quality marginal"
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Query Match
Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12043 TAGATTTGGGCTACAACAATTTCTCGGGACAGTTACCTACTGAAATTTCTCAGATACAGA 12102
                                                                                                                           12283 CAGGAGAAATCCCTCGAGAGATTGGCAACTGCACAAGCCTTTTGTGGTTTAACGTGGCAA 12342
                                                                                                                                                                                                                                                           12223
                                                                                                                                                                                                                                                                                                                                                                                       12163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12103 GTTTGAAGTTCTTGATTCTTGCTTATAATAACTTCAGTGGCGATATACCACAGGAGTATG 12162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
12343 ACAACCAGCTCTCTGGTAGATTCC 12366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sg
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                                                                                                                                                                                                                                                                                                                                                                             gcaatgatttgtgtggaacaatcc 652
                                                                                                                                                                cggggccaatccctagagcactcactgcaatcccaagccttaaagttgttgatgtctcaa 628
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                                                                                                                                                                                                                                                           CAGCTTCATTTGGGAAATTGACCTCTTTTTGTGGCTAATGCTTGCAAACAACTCTCTAT 12282
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GB:AAC49810 (putative receptor protein kinase); contains
Pfam profiles: PF00560 Leucine Rich Repeat (17 repeats),
PF00069 Eukaryotic protein kinase domain"
10992. .14231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9791. .9912
9791. .9912
/note-"exon predicted by xgrail, quality marginal"
10574. .10662
/note-"exon predicted by xgrail, quality good"
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VKASNVLLDKHGNARVTDFGLARLLNVGDSHVSTVIAGTIGYVAPEYGQTWQATTRGD
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/protein_id="AAF15908.1"
/db_xref="GI:6539238"
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Search completed: June 24, 2000, 00:26:34 Job time: 46549 sec

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N W09743427-A1.

P 13-MAY-1997; E02443.

R 14-MAY-1996; GE-010044.

R (NOVS ) NOVARTIS AG.

LOVE VILES SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

De VILES SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

R PPSDB; W47022.

R P-PSDB; W47022.

T Production of apomictic seeds - useful in plant breeding

C Claim 28; Pages 86-88; 123pp; English.

C The sequence is that of an EST clone showing high homology to

C SERK LRR (leucine-rich repeat) sequences.

C SERK LRR (leucine-rich repeat) sequences.

G Sequence 1063 BP; 313 A; 242 C; 206 G; 302 T;
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Best Local :
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V06590;
03-AUG-1998 (first entry)
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST clone.
receptor kinase; apomixis; apomictic; seeds; product
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Arabidopsis thaliana.
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Cf-9 cDNA.
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V06586;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologous EST cl
receptor kinase; apomixis; apomictic; seeds; pr
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Key
CDS 142...798
                                           W09743427-A1
20-N0V-1997; E02443.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, S
WPI; 98-086529/08.
p-PSDB; W47018.

Production of apomictic seeds - useful in plant breeding Claim 28; Pages 71-73; 123pp; English.

The sequence is that of an EST clone showing high homolog SERK LRR (leucine-rich repeat) sequences.
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20-NOV-1997.

13-MAY-1997; E02443.

14-MAY-1996; GB-010044.

(NOVS ) NOVARTIS AG.

De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;

WPI; 98-086529/08.

P-SSDB; W47019.

R P-SSDB; W47019.

Production of apomictic seeds - useful in plant breed Claim 28; Pages 75-77; 123pp; English.

The sequence is that of an EST clone showing high hom SERK LRR (leucine-rich repeat) sequences.

Sequence 981 BP; 286 A; 236 C; 180 G; 2
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V06587;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LAR homologous ES:
receptor kinase; apomixis; apomictic; seeds
plant breeding; leucine-rich repeat; ss.
Arabidopsis thaliana.
Location/Qualifiers
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20-NOV-1997.
13-MAY-1997; E02443.
14-MAY-1996; GB-010044.
(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG, SI
WPI; 98-086529/08.
P-PSDB; W47020.
Production of apomictic si
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                                                                                                                                                                                                                                                                                                                                          Production of apomictic seeds - useful in plant breeding Claim 28; pages 79-80; 123pp; English.
The sequence is that of an EST clone showing high homology SERK LRR (Leucine-rich repeat) sequences.
Sequence 788 BP; 234 A; 191 C; 156 G; 207 T;
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20-NOV-1997.
21-MAY-1997; E02443.
21-MAY-1996; GB-010044.

(NOVS ) NOVARTIS AG.
De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;
WPI; 98-086529/08.

P-SSDB; W47021.
Production of apomictic seeds - useful in plant breed Claim 28; Pages 83-64; 123pp; English.
The sequence is that of an EST clone showing high hom SERK LRR (leucine-rich repeat) sequences.
Sequence 894 BP; 270 A; 163 C; 176 G;
                                                                                                                     Arabidopsis
Key
CDS
                                                                                                                                         V06589;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK LRR homologreceptor kinase; apomixis; apomictic;
plant breeding; leucine-rich repeat;
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Matches 538;
                   V06591;
03-AUG-1998 (first entry)
Arabidopsis thaliana SERK gene.
receptor kinase; apomixis; apomictic;
plant breeding; ds.
Arabidopsis thaliana.
Key
CDS
195..2072
                                                                        V06591 standard;
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                                                                                                                                                                                                                                                                                               TGAACTTGGGAAGCTTGAACATTTACAATATCTGTATGGAATCATCACTCTTTTGCCTTT
                                                                                                                                                                                                                                                                                                                                                            gtgtggaacaatcccaacaacggaccttttgctcacattcctttacagaactttgagaa
                                                                                                                                                                                                                  TCCTAGAGAACTCACAGTTATTTCAAGCCTTAAAGTTGTTGATGTCTCAGGGAATGATTT
                                                                                                                                                                                                                        ccctagagcactcactgcaatcccaagccttaaagttgttgatgtctcaagcaatgattt
                                                                                                                                                                                                                                             GGGAAAATTGAAGTCACTTGTTTTTTGCGGCTTAACGAAAACCGATTGACCGGTCCTAT
                                                                                                                                                                                                                                                  gggaaaattgaagtctctggtctttttacggcttaatgacaaccgattgacggggccaat
                                                                                                                                                                                                                                                                                                                          TGATTATCTGAAAACATTTACATTATCAGTCACACATATAACATTTTGCTTTGAGTCATA
                                                                                                          TACCAAGTGTTTGTAAATC
                                                                                                                      caccactttatcaaatatc
                                                                                                                                                                                        GTGTGGAACAATTCCAGTAGAAGGACCTTTTGAACACATTCCTATGCAAAACTTTGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 34.0%;
Similarity 72.8%;
38; Conservative
     /*tag= a
/product=
                                                                         cDNA to
                                                                                                                      837
                                                                         mRNA;
        SERK
                                              apomictic;
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Pred. No. 2e-91;
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                                               seeds;
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                                               production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.

Seed and forage quality and maturity.

Sequence 2089 BP; 568 A; 419 C; 503 G; 599 T;
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Best Local
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13-MAY-1997;
14-MAY-1996;
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The sequence is that encoding SERK, a putative receptor kinase.
It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG,
WPI; 98-086529/08.
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mes 327; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       aaccaagacaaccgcgtcactcgtgtggatttggggaattcaaacctctctggacatctt
                                            ccttttgctcacattcctttacagaactttgagaacaac 702
                                                                                                 agccttaaagttgttgatgtctcaagcaatgatttgtgtggaacaatcccaacaaacgga
                                                                                                                                       CTCCGGCTTAACAACAACAGTCTCACTGGGTCAATTCCTATGTCACTGACCAATATTACT
                                                                                                                                                           TTAAACAGCTTCTCCGGTCCTATTCCGGAATCATTGGGAAAGCTTTCAAAGCTGAGATTT
                                                                                                                                                                                                                              aacaacaatcttacagggatagttcccacttctttgggaaaattgaagtctctggtcttt
                                                                                                                                                                                                                                                              ACTGGCCCGATTCCTAGTAATCTTGGAAATCTGACAAACTTAGTGAGTTTGGATCTTTAC
                                                                                                                                                                                                                                                                                                                           GTTCCAGAGCTTGGTGTGCTCAAGAATTTGCAGTATTTGGAGCTTTACAGTAACAACATA
                                                                                                                                                                                                                                                                                                                                           gcgcctgagcttgggaagcttgaacatttacagtatctagagctctacaaaaaacaacatc
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                                                                           ACCCTTCAAGTGTTAGATCTATCAAATAACAGACTCTCTGGTTCAGTTCCTGACAATGGC
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GB-010044.
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0; Mismatches 192;
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Pred. No. 1.1e-49;
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Production of apomictic seeds - useful in plant breeding Production of apomictic seeds.

Claim 21; Pages 47-51; 123pp; English.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed appropagated hybrids and could shorten and simplify the breeding programs that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;
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14-MAY-1996; GB-010044.
(NOVS) NOVARTIS AG.
De Vries SC, Hecht VFG, SWPI; 98-086529/08,
P-PSDB; W477013.
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Key
CDS
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03-AUG-1998 (first entry)
Daucus carota SERK gene.
receptor kinase; apomixis; apomictic; seeds; production; embryos;
plant breeding; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                          363 tgcgcctgagcttgggaagcttgaacatttacagtatctagagctctacaaaaacaacat 422
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hes 200;
CTCATTTTCTTTGTTTACACCTATCAGTTTTGCCCAATAATTTGAATTTATGTGGACCCGT
                    CTTGCGTCTCAACAACAACAGCCTCTCTGGTCCAATTCCAATGTCACTGACTAATATTAC
                                                                                                                                                                         CATGAATAGCTTCTCTGGACCTATACCGGACACATTAGGAAAGCTTACAAGGCTAAGATT
                                                                                                                                                                                                                                                                   caacaacaatcttacagggatagttcccacttctttgggaaaattgaagtctctggtctt
                                                                                                                                                                                                                                                                                                          AAGTGGACCAATTCCTAGTGATCTTGGGGAATCTGACAAATTTGGTGAGCTTGGACCTATA
                                                                                                                                                                                                                                                                                                                                ccaaggaactataccttccgaacttggaaatctgaagaatctcatcagcttggatctgta 482
                                                                                                                                                                                                                                                                                                                                                                                      TGATGCTTACCTTGACAAATATGGGGGTTCTTATGACATTGGAGCTTTACAGCAATAACAT 197
                                                                       AACTCTTCAAGTCCTGGATTTATCAAACAATCGGCTATCAGGACCAGTACCGGATAATGG
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Pred. No. 1.8e-19;
0; Mismatches 161
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Best Local S
Matches 169
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The present sequence encodes an Arabidopsis thaliana plant morphogenesis regulatory protein (MRP), which can be used to yie a plant with, e.g. short stems or altered inflorescence. The MRF acts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP; scDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant.

Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;
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x23526;
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24-AUG-1995; JF-216187.
24-AUG-1995; JF-21618.
24-AUG-1995; JF-2
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10-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atttacagtatctagagctctacaaaaacaacatccaaggaactataccttccgaacttg
                                                                                                                                                                                           gcaatgatttgtgtggaacaatccc
                                                                                                                                                                                                                                                GTGGCACTATACCCCGAGCATTTCAAAAGCTAGAAAGTATGACTTACCTTAATCTGTCCA
                                                                                                                                                                                                                                                                                            cggggccaatccctagagcactcactgcaatcccaagccttaaagttgttgatgtctcaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAGCTTACTGACTTGTTTGATCTGAATGTGGCCAACAATGATCTGGAAGGACCTATAC
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                                                                                                                                                  GCAACAATATCAAAGGTCCAATCCC
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169; Conserv
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                            standard;
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/note= "plant morphogenesis regulatory
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Oryza longistaminata.
W09909151-A2.
W09909151-A2.
25-FEB-1999.
17-JUL-1998; U14841.
                             11-MAY-1995; G01075.

11-MAY-1994; GB-009394.

23-DEC-1994; WO-G02812.

31-MAR-1995; GB-006658.

07-APR-1995; GB-007232.

(GATS-) GATSBY CHARITABL
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generating transgenic plants resistant to
Claim 1; Page 52-53; 67pp; English.
This invention describes a method for conf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
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(REGC ) UNIV CALIFORNIA.
Hulbert SH, Richter T, F
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cassava; maize;
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Claim 9; Page 85-87; 131p; English.

T06307 is a tomato pathogen resistance gene Cf-2.2 partial cDNA clone. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.2 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulvum. C.fulvum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 3573 BP; 1032 A; 654 C; 664 G; 1223 T;
23-NOV-1995;
11-MAY-1995;
11-MAY-1994;
11-MAY-1994;
23-DEC-1994;
31-MAR-1995;
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Claim 9; Page 80-83; 131pp; English.

T06306 is the tomato pathogen resistance gene Cf-2.1. In a new method this gene is expressed highly in genetic constructs which may be used to impart a broad range of pathogen resistance, by induction of variegation, to transgenic plants (or parts or propagules of plants) containing such constructs. Cf-2.1 imparts resistance to the disease caused by the leaf mould fungal pathogen Cladosporium fulrum.

C. fulrum contains avirulence (Avr) genes that confer recognition by plants containing Cf-genes, leading to the activation of host defence mechanisms to attack the disease.

Sequence 6471 BP; 2073 A; 1106 C; 1122 G; 2170 T;
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(GATS*) GATSBY CHARITABLE
Hammond-Kosack KE, Jones
WPI; 96-010949/01.
P-PSDB; R85298.
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receptor kinase; apomixis; apomictic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtacaacaacaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACAACTTGTCTATGTTGTATCTTTACAATAATCAGCTTTCTGGCTCTATTCCTGAAGAA
                                                                                                                                                                                                                                                                                                                                                 GTTTTGTCGATGTCATCTAATAGTTTCAGTGGAGAGCTCCCTTCA
                                                                                                                                                                                                                                                                                                                                                               gttgttgatgtctcaagcaatgatttgtgtggaacaatcccaaca
                                                                                                                                                                                                                                                                                                                                                                                                                           CTCATTGGGGAAATTCCTTCATCTGTGTGCAATTTGACATCACTGGAAGTGTTGTATATG
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                                                                                                                                                                                                                                                                                                                                                                                                    CCGAGAAACAATTTGAAGGGAAAAGTTCCGCAATGTTTGGGGTAATATCAGTAACCTTCAG
                                                                                                                                                                                                             breeding; ds.
                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                       /number= 1
3851. .3979
/*tag= c
                     /*tag= c
/number= 2
4124. .4211
/*tag= d
/number= 3
                                                                                                            /note= "contains introns"
3731. .3802
/*tag= b
                                                                                                                                                                                                                                                                              DNA; 4081
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.7%;
50.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 2.
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                                                                                                                                                                                                                          seeds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
.6e-10;
                                                                                                                                                                                                                          production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6471;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                            plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant to reeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed apomictic plant and could shorten and simplify the breeding propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Seed and forage quality and maturity.
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Production of apomictic seeds - useful in plant breeding Claim 26; Pages 64-67; 123pp; Epglish.

The sequence is that encoding SERK, a putative receptor kinase. It may be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing
                                                                                                                                                                                                                                                                   1794
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             03-AUG-1998 (first entry)
Daucus carota SERK gene.
receptor kinase; apomixis;
                                                           V06570 standard; DNA; 6695
V06570;
   plant
                                                                                                                                                                                                                                                                                             195
                                                                                                                                                                   ccgcgtcactcgtgtgga 332
                                                                                                                                                                                                                                                                                   aggagatgctctttacgctcttcgccggagtttaacagatccggaccatgttctccagag
                                                                                                                                                 CAGTGTCATAAGAGTGTA 1931
                                                                                                                                                                                                                         ctgggatccaactcttgttaatccttgtacctggttccatgtcacctgtaaccaagacaa 314
                                                                                                                                                                                                                                                                   AGGTGATGCTTTGCATACTTTGAGGGTTACTCTAGTTGATCCAAACAATGTCTTGCAGAG 1853
                                                                                                                                                                                                         CTGGGATCCTACGCTAGTGAATCCTTGCACATGGTTCCATGTCACTTGCAACAACGAGAA 1913
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   breeding; ds
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GB-010044.
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/*tag= g
/number= 6
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4430..45
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                apomixis; apomictic; seeds; production; embryos;
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Pred. No. 3.2e
0; Mismatches
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.2e-10;
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ctgggatccaactcttgttaatccttgtacctggttccatgtcacctgtaaccaagacaa 314 AGGCGATGCATTACACAACTTACGAACTAGCTTGCAAGATCCCAACAATGTCCTGCAGAG

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Production of apomictic seeds - useful in plant breeding Production of apomictic seeds - useful in plant breeding Scalaim 21; Pages 40-46; 123pp; English.

Claim 21; Pages 40-46; 123pp; English.

Critically be used as part of a method of producing apomictic seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenic; (b) regenerating the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides breeding programs. Controllable and reproducible apomixis provides breeding programs. Apomixis provides for true-breeding, seed apomictic plant. Apomixis provides for true-breeding, seed process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with seed and forage quality and maturity.

Sequence 6695 BP; 1844 A; 1182 C; 1243 G; 2422 T;
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13-MAY-1997;
14-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                     (NOVS ) NOVARTIS AG.

De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ, WPI; 98-086529/08.
P-PSDB; W47013.
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 l Similarity
96; Conserv
 6.7%;
ilarity 69.6%;
Conservative
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3851. .3979
/*tag= c
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/*tag= h
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/*tag= g
/number= 6
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3731. .
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; Score 70.8; D
; Pred. No. 3.9e
0; Mismatches
              DB 1;
1.9e-10;
  42;
                          Length 6695;
  0
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cladosporium fulvum-5. Transgenic plants can be produced by incorporating the gene into plant cells and regenerating plants from the cells; asexually or sexually produced offspring can also be subsequently produced. Expression of the gene in plant cells can confer pathogen resistance on a plant e.g. to tomato leaf mould (C. fulvum) in tomatoes. Oligonucleotides with sequences complementary to the gene or fragments of it, are useful in anti-sense techniques to reduce gene expression. The nucleic acids/polynucleotides are useful as hybridisation probes to identify other genes/fragments conferring pathogen resistance on plants e.g. Phytophthora resistance in potatoes. Homologies between Cf-5 and cf-9 may be used to identify further resistance genes of this class. Sequence 3979 BP; 1217 A; 717 C; 698 G; 1347 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-1996; GB-019924.
24-SEP-1996; GB-019924.
09-MAY-1996; GB-0199881.
(INNE-) INNES CENT INNOVATIONS LTD JOHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Fig la; 75pp; English.

This sequence is an example of the polynucleotide of the invention, is able to confer pathogen resistance on a plant. It is one of two CF-5 gene variants, which offer resistance against the pathogen Cladosporium fulvum-5. Transgenic plants can be produced by incorpo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1076
                                                                2124
                                                                                                                                                                                                                                   2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomato gene Cf-5, confers resistance to Cladosporium fulvum - u for production of transgenic plants resistant to pathogens e.g. tomato leaf mould C. fulvum in tomatoes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF-5 pathogen resistance gene variant #1.
Tomato; CF-5 pathogen resistance gene; Cladosporium fulvum-5;
tomato leaf mould; Phytophthora resistance; ss.
Lycopersicon pimpinellifolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1016
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                                                                                                                                                                                                                                                                                                                1944 AACAACTTGTTTATGTTGTATCTTTACAATAATCAGCTTTCTGGCTCTATTCCTGAAGAA 2003
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ataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtacaacaacaat 492
                                                                                                                                                                                                                                                                      cttgggaagcttgaacatttacagtatctagagctctacaaaaacaacatccaaggaact 432
                                                             CTTTCTGGCTCTATTCCTGCTTCATTTGGCAATATGAGAAATCTGCAAACTCTGTTTCTC
                                                                                                                                             ATTCCTGCTTCATTGGGGAATCTAAACAACTTGTCTAGGTTGTATCTTTACAATAATCAG 2123
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                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                      50.4%;
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Pred. No. 3
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.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                  169;
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ID V14519
AC V14519
AC V14519
AC V14519
DT CF-5 PA
KW TOMATO
KW TOMATO
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09-MAY-1996; GB-009681
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In Tomato gene CG-5, confers resistance to Cladosporium fulvum - useful production of transgenic plants resistant to pathogens e.g. for production of transgenic plants resistant to pathogens e.g. to the production of transgenic plants resistant to pathogens e.g. Claim 6; Fig 1b; 75pp; English.

Produced is an example of the polynucleotide of the invention, and confer pathogen resistance on a plant. It is one of two tomato CC This sequence is an example of the polynucleotide of the pathogen cC CF-5 gene variants, which offer resistance against the pathogen cC Cladosporium fulvum-5. Transgenic plants can be produced by incorporating the gene into plant cells and regenerating plants from the cells; cC asexually or example produced offspring can also be subsequently concluded. Expression of the gene in plant cells can confer pathogen cresistance on a plant e.g. to tomato leaf mould (C. fulvum) in tomatoes. CO ligonucleotides with sequences complementary to the gene or fragments conference actions probes to identify other genes/fragments conference as hybridisation probes to identify other genes/fragments conference as hybridisation probes to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF-5 pathogen resistance gene variant #2.
Tomato; CF-5 pathogen resistance gene; Cladd tomato leaf mould; Phytophthora resistance;
Lycopersicon pimpinellifolium.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identify other genes/fragments conferring pathogen resistance on plants e.g. Phytophthora resistance in potatoes. HomoLogies between Cf-5 and Cf-9 may be used to identify further resistance genes of this class. Sequence 3979 BP; 1218 A; 716 C; 698 G; 1347 T;
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                                             ataccttccgaacttggaaatctgaagaatctcatcagcttggatctgtacaacaat
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AGTGATAACGATCTCATTGGGGAAATTCCTTCATTTGTGTGCAATTTGACATCACTGGAA
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Pred. No. 3.6e-10;
0; Mismatches 169
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